

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:56 ; Search time 9 Seconds

(without alignments)
27.140 Million cell updates/sec

Title: US-09-580-018-7

Perfect score: 54

Sequence: 1 KMDAEFRHDS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents-AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	18	2	US-08-149-975A-3
2	54	100.0	27	1	US-08-141-324-11
3	54	100.0	27	1	US-08-541-502-11
4	54	100.0	45	1	US-08-462-859A-5
5	54	100.0	45	1	US-08-123-659A-5
6	54	100.0	45	1	US-08-464-247A-5
7	54	100.0	45	1	US-08-464-248A-5
8	54	100.0	53	4	US-09-173-887-5
9	54	100.0	58	1	US-08-371-930-25
10	54	100.0	58	5	PCT-US94-01712-25
11	54	100.0	59	1	US-08-484-969-3
12	54	100.0	59	1	US-08-472-627-3
13	54	100.0	59	1	US-08-388-463-3
14	54	100.0	63	1	US-08-462-859A-3
15	54	100.0	63	1	US-08-462-859A-4
16	54	100.0	63	1	US-08-123-659A-3
17	54	100.0	63	1	US-08-123-659A-4
18	54	100.0	63	1	US-08-464-247A-3
19	54	100.0	63	1	US-08-464-247A-4
20	54	100.0	63	1	US-08-464-248A-3
21	54	100.0	63	1	US-08-464-248A-4
22	54	100.0	103	2	US-08-404-831-2
23	54	100.0	103	2	US-08-612-785B-2
24	54	100.0	103	2	US-08-475-579A-2
25	54	100.0	103	2	US-08-920-162A-2
26	54	100.0	103	2	US-08-339-708A-10
27	54	100.0	103	4	US-09-356-931-2

28	54	100.0	103	4	US-08-703-675C-2	Sequence 2, Appl1
29	54	100.0	103	4	US-08-617-267C-2	Sequence 2, Appl1
30	54	100.0	105	2	US-08-729-345-1	Sequence 1, Appl1
31	54	100.0	117	2	US-08-729-345-3	Sequence 3, Appl1
32	54	100.0	152	6	5187153-4	Patent No. 5187153
33	54	100.0	162	6	5220013-4	Patent No. 5220013
34	54	100.0	162	6	5223482-4	Patent No. 5223482
35	54	100.0	264	1	US-07-990-893-5	Sequence 5, Appl1
36	54	100.0	487	1	US-08-462-859A-9	Sequence 9, Appl1
37	54	100.0	487	1	US-08-123-659A-9	Sequence 9, Appl1
38	54	100.0	487	1	US-08-464-247A-9	Sequence 9, Appl1
39	54	100.0	487	1	US-08-464-248A-9	Sequence 9, Appl1
40	54	100.0	492	1	US-08-462-859A-7	Sequence 7, Appl1
41	54	100.0	492	1	US-08-123-659A-7	Sequence 7, Appl1
42	54	100.0	492	1	US-08-464-247A-7	Sequence 7, Appl1
43	54	100.0	492	1	US-08-464-248A-7	Sequence 7, Appl1
44	54	100.0	537	1	US-08-453-552-4	Sequence 4, Appl1
45	54	100.0	537	2	US-08-710-637-4	Sequence 4, Appl1

ALIGNMENTS

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RESULT 1
US-08-149-975A-3
; Sequence 3, Application US/08149975A
; Patent No. 5849600
;
; GENERAL INFORMATION:
; APPLICANT: Nixon, Ralph
; APPLICANT: Honda, Toshiyuki
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,975A
; FILING DATE: 11-NOV-1993
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04843/016001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-149-975A-3
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; Query Match 100.0%; Score 54; DB 2; Length 18;
; Best Local Similarity 100.0%; Pred. No. 0.00015;
; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 KMDAEFRHDS 10
; | | | | | | | | | |
; DB 2 KMDAEFRHDS 11
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RESULT 2
US-08-141-324-11
; Sequence 11, Application US/08141324
; Patent No. 5475097
; GENERAL INFORMATION:
; APPLICANT: Travels, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-141-324-11

Query Match 100.0%; Score 54; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10
DB 7 KMDAEFRHDS 16

RESULT 3
US-08-541-902-11
; Sequence 11, Application US/08541902
; Patent No. 5707620
; GENERAL INFORMATION:
; APPLICANT: Travels, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.

STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,902
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-541-902-11

Query Match 100.0%; Score 54; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10
DB 7 KMDAEFRHDS 16

RESULT 4
US-08-462-859A-5
; Sequence 5, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5652092e1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.

REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-5

Query Match 100.0%; Score 54; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAERRHDS 10
DB 8 KMDAERRHDS 17

RESULT 5
US-08-123-659A-5
Sequence 5, Application US/08123659A
Patent No. 5656477
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-5

Query Match 100.0%; Score 54; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAERRHDS 10
DB 8 KMDAERRHDS 17

RESULT 6
US-08-464-247A-5
Sequence 5, Application US/08464247A
Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-5

Query Match 100.0%; Score 54; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAERRHDS 10
DB 8 KMDAERRHDS 17

RESULT 7
US-08-464-248A-5
Sequence 5, Application US/08464248A
Patent No. 5703209
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-5

Query Match
Best Local Similarity 100.0%; Score 54; DB 1; Length 45;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAFFFFHDS 10
DB 8 KMDAFFFFHDS 17
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RESULT 8
US-09-173-887-5
Sequence 5, Application US/09173887
Patent No. 6245884
GENERAL INFORMATION:
APPLICANT: Hook, Vivian Y.H.
TITLE OF INVENTION: SECRETASES RELATED TO ALZHEIMER'S DEMENTIA
FILE REFERENCE: P-RAS 3337
CURRENT APPLICATION NUMBER: US/09/173,887
CURRENT FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 53
TYPE: PRT
ORGANISM: mammalian
US-09-173-887-5

Query Match
Best Local Similarity 100.0%; Score 54; DB 4; Length 53;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAFFFFHDS 10
DB 2 KMDAFFFFHDS 11
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RESULT 9
US-08-371-930-25
Sequence 25, Application US/08371930
Patent No. 5578451
GENERAL INFORMATION:
APPLICANT: Nishimoto, Ikuo
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,930
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/019,208
FILING DATE: February 18, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/154001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
US-08-371-930-25

Query Match
Best Local Similarity 100.0%; Score 54; DB 1; Length 58;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAFFFFHDS 10
DB 45 KMDAFFFFHDS 54
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RESULT 10
PCT-US94-01712-25
Sequence 25, Application PC/TUS9401712
GENERAL INFORMATION:
APPLICANT: Nishimoto, Ikuo
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/019,208
FILING DATE: February 18, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/154001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 58
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US94-01712-25

Query Match 100.0%; Score 54; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10
DB 45 KMDAEFRHDS 54

RESULT 11

US-08-484-969-3
Sequence 3, Application US/08484969
Patent No. 5679531

GENERAL INFORMATION:

APPLICANT: Konig, Gerhard
TITLE OF INVENTION: Monoclonal Antibody Specific for BA4
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,969
FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 95,216
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: Cleavage-site

LOCATION: 4..5
OTHER INFORMATION: /label= Beta

OTHER INFORMATION: /note= "Beta cleavage site in App"

FEATURE:

NAME/KEY: Cleavage-site

LOCATION: 20..21
OTHER INFORMATION: /label= Alpha

OTHER INFORMATION: /note= "Alpha cleavage site in App, residues 16/17"

FEATURE:

NAME/KEY: Cleavage-site

LOCATION: 46..47
OTHER INFORMATION: /label= Gamma

OTHER INFORMATION: /note= "Gamma cleavage site in App"

NAME/KEY: Peptide

LOCATION: 5..47
OTHER INFORMATION: /label= BA4
OTHER INFORMATION: /note= "BA4 peptide"

FEATURE:

NAME/KEY: Region

LOCATION: 33..56
OTHER INFORMATION: /label= Tm

OTHER INFORMATION: /note= "Transmembrane region of App"

FEATURE:

NAME/KEY: Region

LOCATION: 1..32

OTHER INFORMATION: /label= Ex

OTHER INFORMATION: /note= "N-terminal extracellular part of App"

US-08-484-969-3

Query Match 100.0%; Score 54; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3 KMDAEFRHDS 12

RESULT 12

US-08-472-627-3
Sequence 3, Application US/08472627
Patent No. 5693753

GENERAL INFORMATION:

APPLICANT: Konig, Gerhard
TITLE OF INVENTION: Monoclonal Antibody Specific for BA4
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,627
FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 95,216
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: Cleavage-site

LOCATION: 4..5
OTHER INFORMATION: /label= Beta

OTHER INFORMATION: /note= "Beta cleavage site in App"

FEATURE:

NAME/KEY: Cleavage-site
LOCATION: 20..21

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? OTHER INFORMATION: /label= Alpha
? OTHER INFORMATION: /note= "Alpha cleavage site in App, residues 16/17
? OTHER INFORMATION: of BA4."
? FEATURE:
? NAME/KEY: Cleavage-site
? LOCATION: 46..47
? OTHER INFORMATION: /label= Gamma
? OTHER INFORMATION: /note= "Gamma cleavage site in App"
? FEATURE:
? NAME/KEY: Peptide
? LOCATION: 5..47
? OTHER INFORMATION: /label= BA4
? OTHER INFORMATION: /note= "BA4 peptide"
? FEATURE:
? NAME/KEY: Region
? LOCATION: 33..56
? OTHER INFORMATION: /label= Tm
? OTHER INFORMATION: /note= "Transmembrane region of App"
? FEATURE:
? NAME/KEY: Region
? LOCATION: 1..32
? OTHER INFORMATION: /label= Ex
? OTHER INFORMATION: /note= "N-terminal extracellular part of App"
US-08-472-627-3

Query Match 100.0%; Score 54; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAFFFFHDS 10
DB 3 KMDAFFFFHDS 12

RESULT 13
US-08-388-463-3
? Sequence 3, Application US/08388463
? Patent No. 5786180
? GENERAL INFORMATION:
? APPLICANT: Konig, Gerhard
? APPLICANT: Graham, Paul
? TITLE OF INVENTION: Monoclonal Antibody Specific for BA4
? TITLE OF INVENTION: Peptide
? NUMBER OF SEQUENCES: 3
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Allegratti & Witcoff, Ltd.
? STREET: 10 South Wacker Drive Suite 3000
? CITY: Chicago
? STATE: Illinois
? COUNTRY: USA
? ZIP: 60606
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/388,463
? FILING DATE:
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: McDonnell, John J
? REGISTRATION NUMBER: 26,949
? REFERENCE/DOCKET NUMBER: 95,216
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-715-1000
? TELEFAX: 312-715-1234
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 59 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
```

```

? MOLECULE TYPE: peptide
? FEATURE:
? NAME/KEY: Cleavage-site
? LOCATION: 4..5
? OTHER INFORMATION: /label= Beta
? OTHER INFORMATION: /note= "Beta cleavage site in App"
? FEATURE:
? NAME/KEY: Cleavage-site
? LOCATION: 20..21
? OTHER INFORMATION: /label= Alpha
? OTHER INFORMATION: /note= "Alpha cleavage site in App, residues 16/17
? OTHER INFORMATION: of BA4."
? FEATURE:
? NAME/KEY: Cleavage-site
? LOCATION: 46..47
? OTHER INFORMATION: /label= Gamma
? OTHER INFORMATION: /note= "Gamma cleavage site in App"
? FEATURE:
? NAME/KEY: Peptide
? LOCATION: 5..47
? OTHER INFORMATION: /label= BA4
? OTHER INFORMATION: /note= "BA4 peptide"
? FEATURE:
? NAME/KEY: Region
? LOCATION: 33..56
? OTHER INFORMATION: /label= Tm
? OTHER INFORMATION: /note= "Transmembrane region of App"
? FEATURE:
? NAME/KEY: Region
? LOCATION: 1..32
? OTHER INFORMATION: /label= Ex
? OTHER INFORMATION: /note= "N-terminal extracellular part of App"
US-08-388-463-3

Query Match 100.0%; Score 54; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAFFFFHDS 10
DB 3 KMDAFFFFHDS 12

RESULT 14
US-08-462-859A-3
? Sequence 3, Application US/08462859A
? Patent No. 5652092
? GENERAL INFORMATION:
? APPLICANT: Jacobsen, J. S.
? APPLICANT: Vittek, M. P.
? TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
? TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate formation
? TITLE OF INVENTION: of B-Amyloid Peptide
? NUMBER OF SEQUENCES: 19
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: American Cyanamid Company
? STREET: One Cyanamid Plaza
? CITY: Wayne
? STATE: New Jersey
? COUNTRY: United States
? ZIP: 07470-8426
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/462,859A
? FILING DATE: 05-JUN-1995
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Barnhard, Elizabeth M.
? REGISTRATION NUMBER: 31,088
```

REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-3

Query Match 100.0%; Score 54; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAERRHDS 10
|||||
Db 8 KMDAERRHDS 17

RESULT 15

US-08-462-859A-4
Sequence 4, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: NO. 5652092el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-4

Query Match 100.0%; Score 54; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAERRHDS 10
|||||
Db 8 KMDAERRHDS 17

Search completed: October 29, 2002, 10:32:08
Job time : 9 secs

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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	47	100.0	10	22	AAB46205	Human APP derived
2	47	100.0	16	21	AAB06315	Human beta-amyloid
3	47	100.0	18	22	AAE00068	Beta-amyloid precu
4	47	100.0	20	21	AAV63713	Beta-APP alpha-sec
5	47	100.0	33	20	AAW96802	Amyloid precursor
6	47	100.0	39	21	AAV63712	Beta-APP alpha-sec
7	47	100.0	45	18	AAW26512	Amyloid precursor
8	47	100.0	45	18	AAW26392	Amyloid precursor
9	47	100.0	45	19	AAW44738	APP-REP 751 (BAP
10	47	100.0	45	19	AAW42977	Deletion beta-amy
11	47	100.0	53	16	AAW64168	Variant beta amylo

12	47	100.0	57	21	AAH10910	Human amyloid precursor
13	47	100.0	58	15	AAH89937	Amyloid precursor
14	47	100.0	63	18	AAW26511	Amyloid precursor
15	47	100.0	63	18	AAW26391	Amyloid precursor
16	47	100.0	63	19	AAW44747	APP-RP 751 PAP peptide
17	47	100.0	63	19	AAW44746	APP-RP 751 PAP peptide
18	47	100.0	63	19	AAW42975	Beta-amyloid peptide
19	47	100.0	63	19	AAW42976	Beta-amyloid peptide
20	47	100.0	67	19	AAW71377	Peptide derived from
21	47	100.0	93	22	AAH919083	Novel human diagnostic
22	47	100.0	112	17	AAH93556	Familial Alzheimer
23	47	100.0	115	20	AAW97999	London-FAD APP polypeptide
24	47	100.0	152	9	AAH83151	Deduced sequence 1
25	47	100.0	162	12	AAH10023	Beta-amyloid-related
26	47	100.0	162	12	AAH37863	Deduced from clone
27	47	100.0	249	15	AAH65798	Beta-amyloid precursor
28	47	100.0	264	10	AAH90497	Protein sequence 1
29	47	100.0	264	10	AAH90609	Sequence of amy 37
30	47	100.0	487	18	AAW26510	Amyloid precursor
31	47	100.0	487	18	AAW26394	Amyloid precursor
32	47	100.0	487	18	AAW44745	APP-RP 751 peptide
33	47	100.0	487	19	AAW44746	Amyloid precursor
34	47	100.0	487	19	AAW42979	Amyloid precursor
35	47	100.0	492	14	AAH45229	APP-RP 751 amyloid
36	47	100.0	492	18	AAW26509	Amyloid precursor
37	47	100.0	492	18	AAW26393	Amyloid precursor
38	47	100.0	492	19	AAW44744	APP-RP 751 peptide
39	47	100.0	492	19	AAW42978	Amyloid precursor
40	47	100.0	536	15	AAH65797	Amyloid precursor
41	47	100.0	627	21	AAH10955	SEAP/human amyloid
42	47	100.0	651	15	AAH65796	Beta-amyloid precursor
43	47	100.0	656	15	AAH65935	Amyloid precursor
44	47	100.0	670	15	AAH67955	APP751 beta-amyloid
45	47	100.0	696	15	AAH89936	Amyloid precursor
			696	9	AAH81092	Sequence of human

ALIGNMENTS

```

RESULT 1
AAB46205
ID AAB46205 standard; peptide; 10 AA
xx

```

DT 04-APR-2001 (first entry)
 YV

Human APP derived immunogenic peptide #1.

KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.

OS Homo sapiens.

PN W0200072880-A2.

07-DEC-2000

PF 26-MAY-2000; 2000WO-US14810.

PR 28-MAY-1999; 99US-0322289.

PA (NEUR-) NEURALAB LTD.

PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
xy

DR WPI; 2001-032104/04
xy

PT preventing or treating a disease associated with amyloid deposits, especially Alzheimer's disease

PT specific antibody -
XY

PS Disclosure; Figure 19: 143pp: English.

CC This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient which comprises:
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta1-3 to 7, in a agent
 CC that induces an immunogenic response against residues 1-3 to 7, in a agent
 CC Abeta. The products of the invention have neurotropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.

SO Sequence 10 AA:

Query Match 100.0%; Score 47; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0053;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEYKMDA 10
 |||||
 DB 1 EISEYKMDA 10

RESULT 2
 ID AAB06315
 AAB06315 standard; peptide: 16 AA.

XX AAB06315;
 XX
 AC AAB06315;
 XX
 DT 03-OCT-2000 (first entry)
 XX
 DE Human beta-amyloid precursor protein beta-secretase cleavage site.
 XX
 KW Human; beta-amyloid precursor protein; beta-APP; beta-secretase;
 KW subtilisin-kexin isoenzyme 1; SKI-1;
 KW pro-brain-derived neurotrophic factor; proBDNF; anti11pemic;
 KW cytosolic; vasotropic; SKI-1 inhibitor; hypercholesterolemia;
 KW liver steatosis; Ras-dependent cancer; restenosis;
 KW amyloid protein formation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FH Cleavage-site 8..9
 PN WO200026348-A2.
 XX
 PD 11-MAY-2000.
 XX
 PP 04-NOV-1999; 99WO-CA01058.
 XX
 PR 04-NOV-1998; 98CA-2249648.
 XX
 PA (RECL-) INST RECH CLINIQUES MONTREAL.
 XX
 PI Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;
 DR WPI: 2000-365601/31.
 XX
 PT Novel soluble proteic fragment of subtilisin-kexin isoenzyme for
 PT producing a polypeptide useful for treating hypercholesterolemia, liver
 PT steatosis and amyloidosis, comprises a specific amino acid sequence -
 XX
 PS Example 4; Page 51; 119pp: English.

CC The present sequence is the beta-secretase site of human beta-amyloid
 CC precursor protein (beta-APP). The sequence may be cleaved
 CC by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1
 CC (SKI-1), a type-I membrane-bound proteinase. Peptides which bind to and

CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for
 CC screening inhibitors of SKI-1 activity, or for screening enhancers of
 CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1
 CC catalytic site may be used as inhibitors of SKI-1 activity. They may be
 CC used to treat diseases involving overexpression of SKI-1 or SKI-1
 CC substrate. Such diseases include hypercholesterolemia, high levels of
 CC fatty acids, lipids or larnesyl pyrophosphate, liver steatosis,
 CC Ras-dependent cancer, restenosis and amyloid protein formation.

SO Sequence 16 AA:

Query Match 100.0%; Score 47; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0089;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEYKMDA 10
 |||||
 DB 1 EISEYKMDA 10

RESULT 3
 ID AAE00608
 AAE00608 standard; peptide: 18 AA.

XX AAE00608;
 XX
 AC AAE00608;
 XX
 DN 02-JUL-2001 (first entry)
 XX
 DE Beta-amyloid precursor protein beta-secretase cleavage site.
 XX
 KW Beta-amyloid precursor protein; beta-APP; caspase; beta-secretase;
 KW cysteine protease; apoptosis; caspase expression cassette; metastasis;
 KW tumour; cathepsin B; ironinase; proliferation; gene therapy;
 KW interdomain linker; cleavage site; Alzheimer's disease.
 XX
 OS Unidentified.
 XX
 PN WO200129232-A2.
 XX
 PD 26-APR-2001.
 XX
 PP 19-OCT-2000; 2000WO-US28941.
 XX
 PR 20-OCT-1999; 99US-0160559.
 XX
 PR 14-AUG-2000; 2000US-0225564.
 XX
 PA (SCIO-) SCIOS INC.
 XX
 PI Cordell B, Li Y;
 DR WPI: 2001-290920/30.
 XX
 PT Novel fusion polypeptide comprising first and second caspase subunit
 PT separated by cleavage site not associated in nature with caspase
 PT subunit, useful for cloning gene encoding enzymes involved in
 PT proteolytic cleavage -
 XX
 PS Example 2; Page 26; 116pp: English.

CC The present sequence is a beta-secretase cleavage site of beta-amyloid
 CC precursor protein (beta-APP). This sequence is used to construct
 CC an artificially engineered chimeric cassette comprising human caspase-3
 CC with interdomain linker replaced by swedish mutant beta-secretase
 CC cleavage site. This modified caspase-3 plays a pivotal role in
 CC Alzheimer's disease. Caspases are a family of cysteine proteases, that
 CC participate in the initiation and execution of apoptosis.
 CC The present invention relates to a method for functional cloning of genes
 CC encoding proteins or enzymes involved in proteolytic cleavage. The
 CC invention is based on the use of caspase expression cassettes comprising
 CC the coding sequence of a proteolytic cleavage site flanked by sequences
 CC encoding two caspase subunits. A fusion polypeptide comprising a first
 CC and a second caspase subunit, separated by a cleavage site not associated
 CC in nature, is useful for cloning gene encoding enzymes involved in

```

CC proteolytic cleavage. An expression cassette containing fusion
CC polypeptide is used to identify a mutant cell line deficient in an
CC enzyme of interest and is also useful for diagnosis and suppression of
CC proliferation or metastases of a tumour cell characterised by
CC overexpression of a polypeptide (e.g. Cathepsin B or urokinase,
CC selectively expressed in the tumour cells). DNA encoding fusion
CC polypeptide is used in gene therapy.
XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 47; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10
Db 3 EEISEVKMDA 12

RESULT 4
AAV69713 standard; peptide: 20 AA.
XX
AC AAV69713;
XX
DT 11-APR-2000 (first entry)
XX
DE Beta-ApP alpha-secretase substrate [KM]-APP(-10,+10).
XX
KW Neurotropic; neuroprotective; beta-amyloid precursor protein; metabolism;
KM cleavage site; beta-secretase; neurodegenerative disease;
KN Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO964587-A1.
XX
PD 16-DEC-1999.
XX
PF 04-JUN-1999; 99WO-FR01326.
XX
PR 05-JUN-1998; 98FR-0007068.
XX
PR 31-MAR-1999; 99US-0122599.
XX
PA (RHON ) RHONE-POULENC ROHER SA.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
XX
WPI: 2000-097537/08.
XX
DR Polypeptide with beta-secretase activity, specific for wild-type
XX amyloid precursor protein, useful in treating Alzheimer's disease
XX
PS Example 3; Page 24; 44pp; French.
XX
CC Peptides AAV69702-Y69718 represent synthetic peptide substrates for a
CC novel polypeptide with beta-secretase activity that can cleave
CC specifically the natural beta-amyloid precursor protein (bAPP). Normal
CC cleavage of the protein occurs between amino acids Met596-Asp597 and
CC Val636-Ile637 (positions 4-5 and 44-45 of AAV69701). The novel
CC polypeptide is used to identify agents that interact specifically with
CC it. These agents regulate metabolism of APP particularly they slow down
CC or reduce production of beta-amyloid, so can be used to treat
CC neurodegenerative diseases, particularly Alzheimer's disease.
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 47; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10

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```

Db 3 EEISEVKMDA 12
XXXXXXXXXXXX

RESULT 5
AAW98002
ID AAW98002 standard; Protein: 33 AA.
XX
AC AAW98002;
XX
DT 21-JUN-1999 (first entry)
XX
DE Amyloid precursor protein (aa656-678) with Swedish mutation.
XX
KW Amyloid precursor protein; APP; human; gene targeting;
KW homologous recombination; transgenic mouse; transgenic animal;
KW animal model; Alzheimer's disease.
XX
OS Mus musculus.
XX
PN WO9909150-A1.
XX
PD 25-FEB-1999.
XX
PF 18-AUG-1997; 97WO-US14507.
XX
PR 18-AUG-1997; 97WO-US14507.
XX
PA (FARB ) BAYER CORP.
XX
PI Wlrak DO;
XX
WPI: 1999-181029/15.
XX
DR Modification of target nucleic acids - by homologous recombination,
XX used particularly for introducing a humanised amyloid precursor
XX protein gene into rodents for producing models of Alzheimer's
XX disease
XX
PS Disclosure: Page 145; 209pp; English.
XX
CC This polypeptide comprises residues 656-678 of a murine amyloid
XX precursor protein (APP). The invention provides a novel gene or
XX targeting strategy that facilitates the introduction of one or
XX more specific mutations into any gene in a single double reciprocal
XX homologous recombination step. The method has been used
XX particularly for introducing a humanised APP gene into rodents for
XX producing animal models of Alzheimer's disease (AD). 4 independent
XX lines of transgenic mice (lines ES5007, ES5103, ES5401 and ES5403)
XX have been created using the gene targeting technique applied to
XX embryonic stem cells. In each line, the mouse APP gene was modified
XX to encode a mouse/human hybrid (m/hAPP) where amino acid residues
XX 666-770 of APP770 were encoded by human cDNA sequences instead of
XX mouse genomic exons (exons 16-18). Within these residues, only 3
XX amino acid differences exist between the mouse and human proteins,
XX i.e. Gly-676 to Arg, Phe-681 to Thr and Arg-684 to His. The
XX exon-cDNA fusion gene therefore encodes an APP containing a
XX humanised beta-amyloid domain. Swedish- and/or London-PAD APP
XX mutations have also been introduced (see also AAW97997-W98001).
XX
SQ Sequence 33 AA;
Query Match 100.0%; Score 47; DB 20; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10
Db 9 EEISEVKMDA 18

RESULT 6
AAV69717

```

```

ID  AAY69717 standard; peptide: 39 AA.
XX
AC  AAY69717;
XX
DT  11-APR-2000 (first entry)
XX
DE  Beta-ApP alpha-secretase substrate [KM]-APP(-20,+20).
XX
KW  Neurotrophic; neuroprotective; beta-amyloid precursor protein; metabolism;
KW  cleavage site; beta-secretase; neurodegenerative disease;
KW  Alzheimer's disease.
XX
OS  Homo sapiens.
XX
PN  M09964587-A1.
XX
PD  16-DEC-1999.
XX
PE  04-JUN-1999; 99MO-FR01326.
XX
PR  05-JUN-1998; 98FR-0007068.
PR  31-MAR-1999; 99US-0122599.
XX
PA  (RHON ) RHONE-POULENC RORER SA.
PA  (URPA-) UNIV CURIE PARIS VI P & M.
PI  RhoIam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
PI  WPI: 2000-097537/08.
XX
DR  WPI: 2000-097537/08.
XX
PT  Polypeptide with beta-secretase activity, specific for wild-type
PT  amyloid precursor protein, useful in treating Alzheimer's disease -
XX
PS  Example 3; Page 24; 44pp; French.
XX
CC  Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
CC  novel polypeptide with beta-secretase activity that can cleave
CC  specifically the natural beta-amyloid precursor protein (BAP). Normal
CC  cleavage of the protein occurs between amino acids Met596-Asp597 and
CC  Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
CC  polypeptide is used to identify agents that interact specifically with
CC  it. These agents regulate metabolism of APP, particularly they slow down
CC  or reduce production of beta-amyloid, so can be used to treat
CC  neurodegenerative diseases, particularly Alzheimer's disease.
XX
SQ  Sequence 39 AA:
Query Match 100.0%; Score 47; DB 21; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EISEYVKMDA 10
DB 12 EISEYVKMDA 21
RESULT 7
ID AAY26512 standard; Peptide: 45 AA.
XX
AC AAY26512;
XX
DT 06-JAN-1998 (first entry)
XX
DE Amyloid precursor protein fragment APP-REP 751 (BAP del11-28).
XX
KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KW substrate; mutelin; secretase; Alzheimer's disease; human.
XX
OS Chimeric Homo sapiens.
XX
OS Chimeric synthetic.
XX
PH Key Location/Qualifiers

```

```

FT Cleavage-site 7..8
FT /note= "secretase cleavage site"
FT Peptide 10..33
FT /label= BAP(del11-28)
FT /note= "truncated beta-amyloid protein"
FT Domain 20..42
FT /label= Transmembrane
XX
PN US5656477-A.
XX
PD 12-AUG-1997.
XX
PE 01-MAY-1992; 92US-0877675.
XX
PR 20-SEP-1993; 93US-0123659.
PR 01-MAY-1992; 92US-0877675.
XX
PA (AMCY ) AMERICAN CYANAMID CO.
PI Jacobsen JS, Vittek MP;
PI WPI: 1997-414594/38.
XX
DR WPI: 1997-414594/38.
XX
PT Nucleic acid encoding amyloid precursor mutelin(s) - comprising
PT reporter gene and coding sequence, for identifying compounds which
PT modify the activity of proteolytic enzymes which cleave APP
XX
PS Disclosure: Fig 5A: 84pp; English.
XX
CC This peptide sequence shows the region of amyloid precursor protein
CC (APP) that includes a truncated beta-amyloid protein (BAP) lacking
CC the native secretase cleavage/recognition site. In an attempt to
CC engineer an APP non-cleavable substrate for secretase, an
CC APP-reporter (APP-RBP) protein that carries the BAP deletion has
CC been expressed in recombinant host cells. Deletion of these 18
CC amino acids, however, still resulted in the secretion of APP.
CC N-terminal APP-reporter fragment into the cytoplasm. Non-
CC cleavable APP substrates can be used to detect other putative
CC abnormal APP processing events. They can also be used to
CC investigate cellular post-translational modifications to APP in
CC order to determine the potential influence on normal secretase and
CC abnormal BAP 'clipping' activities.
XX
SQ Sequence 45 AA:
Query Match 100.0%; Score 47; DB 18; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EISEYVKMDA 10
DB 2 EISEYVKMDA 11
RESULT 8
ID AAY26392 standard; Peptide: 45 AA.
XX
AC AAY26392;
XX
DT 15-DEC-1997 (first entry)
XX
DE Amyloid precursor protein fragment APP-REP 751 (BAP del11-28).
XX
KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KW substrate; mutelin; secretase; Alzheimer's disease; human.
XX
OS Chimeric Homo sapiens.
XX
OS Chimeric synthetic.
XX
PH Key Location/Qualifiers
FT Cleavage-site 7..8
FT /note= "secretase cleavage site"

```



```

FT Peptide 10..33
FT /label= BAP(delta11-28)
FT /note= "truncated beta-amyloid protein"
FT Domain 20..42
FT /label= Transmembrane
XX
XX US5652092-A.
XX
XX 29-JUL-1997.
XX
XX 01-MAY-1992; 92US-0877675.
XX
XX 20-SEP-1993; 93US-0123659.
XX 01-MAY-1992; 92US-0877675.
XX 05-JUN-1995; 95US-0462859.
XX
XX (AMCY ) AMERICAN CYANAMID CO.
XX
XX Jacobson JS, Vittek MP;
XX
XX WPI: 1997-392937/36.
XX
XX Screening for compounds which reduce beta-amyloid protein formation
XX - using cells which express a construct encoding a marker and an
XX amyloid precursor muttein derived from APP isoforms
XX
XX PS Disclosure; Fig 5A; 84pp; English.
XX
XX CC This peptide sequence shows the region of amyloid precursor protein
XX (APP) that includes a truncated beta-amyloid protein (BAP) lacking
XX the native secretase cleavage/recognition site. In an attempt to
XX engineer an APP non-cleavable substrate for secretase, an
XX APP-reporter (APP-REP) protein that carries the BAP deletion has
XX been expressed in recombinant host cells. Deletion of these 18
XX amino acids, however, still resulted in the secretion of an
XX N-terminal APP-reporter fragment into the cytoplasm. Non
XX cleavable APP substrates can be used to detect other putative
XX abnormal APP processing events. They can also be used to
XX investigate cellular post-translational modifications to APP in
XX order to determine the potential influence on normal secretase and
XX abnormal BAP 'clipping' activities.
XX
XX SQ Sequence 45 AA:
XX
XX Query Match 100.0%; Score 47; DB 18; Length 45;
XX Best Local Similarity 100.0%; Pred. No. 0.028;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EEISEVKMDA 10
XX |||||
XX 2 EEISEVKMDA 11
XX
XX RESULT 9
XX ID AAM44748 standard; Protein: 45 AA.
XX
XX AC AAM44748;
XX
XX DT 01-JUN-1998 (first entry)
XX
XX DE APP-REP 751 [BAP delta(11-28)] peptide.
XX
XX KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
XX KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
XX KW Alzheimer's disease; cleavage.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX FH Cleavage-site 7..8
XX FT /note= "putative secretase cleavage site"

```

```

FT Misc-difference 19..20
FT /note= "residues 11-28 of the wild type BAP sequence
FT are deleted from between these positions"
XX
XX US5693478-A.
XX
XX 02-DEC-1997.
XX
XX 05-JUN-1995; 95US-0464247.
XX
XX 20-SEP-1993; 93US-0123659.
XX 01-MAY-1992; 92US-0877675.
XX 05-JUN-1995; 95US-0464247.
XX
XX (AMCY ) AMERICAN CYANAMID CO.
XX
XX Jacobson JS, Vittek MP;
XX
XX WPI: 1998-031744/03.
XX
XX Amyloid precursor muttein reporter molecule assay containing antibody
XX recognised marker - used to study pathways associated with
XX Alzheimer's disease
XX
XX PS Disclosure; Fig 5A; 84pp; English.
XX
XX CC This sequence represent the beta-amyloid protein sequence from the
XX construct APP-REP751 [BAP delta(11-28)]. The mutant sequence contains
XX a deletion of the wild type BAP residues 11-28. This causes a
XX shortening of the BAP sequence. This may affect cleavage of the BAP by
XX the "secretase" dependent on whether the "secretase" recognizes the
XX cleavage site by a positional effect or by sequence. The mutant sequence
XX can be used in a method to study secretase and beta-amyloid protein
XX (BAP) generating pathways associated with Alzheimer's disease by
XX studying proteolytic cleavage of the reporter polypeptides (e.g.
XX AAM44744 and AAM44745).
XX
XX SQ Sequence 45 AA:
XX
XX Query Match 100.0%; Score 47; DB 19; Length 45;
XX Best Local Similarity 100.0%; Pred. No. 0.028;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EEISEVKMDA 10
XX |||||
XX 2 EEISEVKMDA 11
XX
XX RESULT 10
XX ID AAM42977 standard; peptide; 45 AA.
XX
XX AC AAM42977;
XX
XX DT 01-MAY-1998 (first entry)
XX
XX DE Deletion beta-amyloid peptide (BAP) derived from APP-REP 751.
XX
XX KW Beta-amyloid peptide; BAP; extracellular BAP plaque;
XX KW cerebrovascular deposit; Alzheimer's disease; Downs syndrome;
XX KW amyloid precursor protein; APP; secretase; BAP aggregation;
XX KW abnormal proteolytic cleavage.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH Domain 20..43
XX FT /note= "putative transmembrane domain"
XX
XX US5703209-A.
XX
XX 30-DEC-1997.

```

PF 05-JUN-1995; 95US-0464248.
 XX 20-SEP-1993; 93US-0123659.
 PR 01-MAY-1992; 92US-0877675.
 XX
 XX
 PA (AMCY) AMERICAN CYANAMID CO.
 XX
 PI Jacobsen JS, Vitek MP;
 XX
 DR WPI: 1998-076482/07.
 XX
 PM Amyloid precursor protein fusion polypeptides - comprising APP
 fragment and marker, useful for research and drug screening
 XX
 PS Disclosure; Fig 5A; 84pp; English.
 XX
 CC The present sequence represents a beta-amyloid peptide (BAP), with
 CC a deletion amino acids 11-28 (numbered according to AAM42976). Abnormal
 CC accumulation of extracellular BAP in plaques and cerebrovascular
 CC deposits is characteristic in brains of individuals suffering from
 CC Alzheimer's disease and Down's syndrome. BAP is a poorly soluble,
 CC self-aggregating protein which is derived from a larger amyloid precursor
 CC protein (APP). APP is expressed as an integral membrane protein, and is
 CC cleaved by secretase, between BAP 16lys and 17leu. Cleavage at this site
 CC precludes amyloidogenesis and results in the release of the
 CC amino-terminal APP fragment. Three major isoforms of APP exist: APP-695,
 CC APP-751 and APP-770. These isoforms are derived by alternative splicing.
 CC APP-APP 751 is a deletion construct of APP-751, which has a deletion of
 CC 276 amino acids to within 15 amino acids of the BAP domain. APP can be
 CC used as a substrate for studying abnormal proteolytic cleavage which
 CC results in the release of BAP, and also to screen for drugs that will
 CC inhibit such cleavage.
 XX
 SQ Sequence 45 AA:
 Query Match 100.0%; Score 47; DB 19; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.028; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;
 QY 1 EEISEVKMDA 10
 Db 2 EEISEVKMDA 11
 |||||||
 RESULT 11
 AAR64168
 ID AAR64168 standard; peptide: 53 AA.
 XX
 AC AAR64168;
 XX
 DT 02-AUG-1995 (first entry)
 XX
 DE Variant beta amyloid protein with 10 preceeding amino acids of APP.
 XX
 KW beta amyloid protein; mutant; variant; detection; amyloid deposition;
 KW diagnosis; amyloidosis associated disease; Alzheimer's disease;
 KW Down's syndrome; APP; amyloid precursor protein.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..10
 FT /note= "the preceeding 10 amino acids of APP"
 FT 11..53
 FT Peptide /note= "beta amyloid protein variant"
 XX
 XX W09428412-A.
 XX
 PD 08-DEC-1994.
 XX
 PF 27-MAY-1994; 94WO-US05809.
 XX
 PR 28-MAY-1993; 93US-0069010.

XX
 PA (MIRI-) MIRIAM HOSPITAL.
 XX
 PI MaJoche RE, Marotta CA;
 XX
 DR WPI: 1995-023013/03.
 XX
 PT Amyloid binding composition comprising labelled amyloid protein
 PT and carrier useful for in vivo imaging of amyloid deposits, for
 PT diagnosing Alzheimer's disease and Down's Syndrome.
 XX
 PS Claim 5; Page 43; 58pp; English.
 XX
 CC AAR64168 shows the amino acid sequence of the beta amyloid protein
 CC plus the 10 amino acids preceeding the amyloid precursor protein. The
 CC protein binds amyloid and is useful for in vivo imaging of amyloid
 CC deposits and hence diagnosis of an amyloidosis-associated disease, such
 CC as Alzheimer's disease or Down's syndrome. AAR64165 shows the generic
 CC sequence of the amyloid protein for generation of variants.
 XX
 SQ Sequence 53 AA:
 Query Match 100.0%; Score 47; DB 16; Length 53;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEISEVKMDA 10
 Db 3 EEISEVKMDA 12
 |||||||
 RESULT 12
 AAB10910
 ID AAB10910 standard; peptide: 57 AA.
 XX
 AC AAB10910;
 XX
 DT 30-JAN-2001 (first entry)
 XX
 DE Human amyloid precursor APP770 A-beta1-40/42 protein fragment.
 XX
 KW APP; amyloid precursor protein; APP770; human; copper agonist; treatment;
 KW amyloid-Abeta-peptide; neurotropic; neuroprotective; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN DE1909357-A1.
 XX
 PD 07-SEP-2000.
 XX
 PF 03-MAR-1999; 99DE-1009357.
 XX
 PR 03-MAR-1999; 99DE-1009357.
 XX
 PA (MULF/) MULTHAUP G,
 PA (BEYR/) BEYREUTHER K.
 XX
 PI Beyreuther K, Multhaup G, Masters CL;
 XX
 DR WPI: 2000-595035/57.
 XX
 PT Copper agonist binds to the copper binding site of amyloid precursor
 PT protein, useful for treating Alzheimer's disease -
 XX
 PS Example 1; Fig 1; 14pp; German.
 XX
 CC This invention describes a novel copper agonist (I) capable of binding to
 CC the copper binding site of an amyloid precursor protein (APP) and/or
 CC preventing or reducing the release of amyloid-Abeta-peptides. The
 CC invention also describes (I) a medicament comprising (I) in combination
 CC with a carrier; (2) identifying (I), comprising: (a) contacting potential
 CC (I) with APP; and (b) detecting a reduction of Abeta-proteins; and (3)
 CC identifying (I) comprising: (a) contacting APP or the copper-binding

CC site-carrying fragment with a solution of, immobilized substance
 CC libraries of, or low molecular weight substances from microorganisms or
 CC plants; (b) performing a competitive assay by adding copper ions to form
 CC complexes with the ligands; (c) identifying the ligands; and (d)
 CC selecting ligands, which bind the APP copper binding site or which reduce
 CC the Abeta peptide release. The products of the invention have neurotropic
 CC and neuroprotective activity. (I) and the resulting medicament are used
 CC for preventing or treating Alzheimer's disease.

XX Sequence 57 AA;

Query Match 100.0%; Score 47; DB 21; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.036;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDA 10
 |||||||||
 DB 6 EISEVKMDA 15

RESULT 13

AAR58937 standard; peptide; 58 AA.

XX AAR58937;

XX 15-APR-1995 (first entry)

XX Amyloid precursor protein residues 551-608.

XX Amyloid precursor protein; beta amyloid; monoclonal antibody;

XX Anti-Alz 90; Alzheimer's disease.

XX Homo sapiens.

XX WO9419692-A.

XX 01-SEP-1994.

XX 17-FEB-1994; 94WO-US01712.

XX 18-FEB-1993; 93US-0019208.

XX (GENO) GEN HOSPITAL CORP.

XX Nishimoto I;

XX WPI; 1994-294486/36.

XX Identifying cpds. useful for treating or preventing Alzheimer's
 PT disease - by determining whether it interferes with the
 PT association of the couplone portion of amyloid precursor protein
 PT to G polypeptide

XX Disclosure; Page 40-41; 71pp; English.

XX Beta amyloid is synthesised as part of a larger protein referred to
 CC as amyloid precursor protein (APP) which has a number of isoforms
 CC in humans, including APP695 and APP770. APP forms a complex with Go,
 CC a GTP-binding protein (or "G protein") in brain. It is suggested
 CC that abnormal APP-GO signalling is involved in the Alzheimer's
 CC disease process. Anti-Alz 90 is a mouse monoclonal antibody
 CC specific for an epitope corresp. to residues 551-608 of APP,
 CC a section of APP that is within the extracellular domain.

XX Sequence 58 AA;

Query Match 100.0%; Score 47; DB 15; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.037;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDA 10
 |||||||||

DB 39 EISEVKMDA 48

RESULT 14

AAW26511 standard; Peptide; 63 AA.

XX AAW26511;

XX 06-JAN-1998 (first entry)

XX Amyloid precursor protein fragment APP-REP 751 (BAP E220).

XX Amyloid precursor protein; APP; beta-amyloid protein; BAP;

XX substrate; multien; secretase; Alzheimer's disease;

XX hereditary cerebral haemorrhage with amyloidosis; human.

XX Homo sapiens.

XX Key

XX Peptide

XX Location/Qualifiers
 10..51
 /label= BAP(E220)
 /note= "beta-amyloid protein E220 mutant"
 25..26
 /note= "secretase cleavage site"
 38..61
 /label= Transmembrane

XX US5656477-A.

XX 12-AUG-1997.

XX 01-MAY-1992; 92US-0877675.

XX 20-SEP-1993; 93US-0123659.

XX 01-MAY-1992; 92US-0877675.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobsen JS, Vitek MP;

XX WPI; 1997-414594/38.

XX Nucleic acid encoding amyloid precursor muten(s) - comprising
 PT reporter gene and coding sequence, for identifying compounds which
 PT modify the activity of proteolytic enzymes which cleave APP
 PT
 XX Disclosure; Fig 5A; 84pp; English.

XX This peptide sequence shows the region of amyloid precursor protein
 CC (APP) that includes a beta-amyloid protein (BAP) carrying a point
 CC mutation (BAP E220) found in patients with hereditary cerebral
 CC haemorrhage with amyloidosis of Dutch origin (HCHMA-D). In an
 CC attempt to engineer an APP non-cleavable substrate for secretase,
 CC an APP-reporter (APP-REP) protein that carries the E22Q mutation
 CC has been expressed in recombinant host cells. This resulted in the
 CC secretion of an N-terminal fragment indistinguishable from that of
 CC APP-REP 751 (see AAW26393-94). Non-cleavable APP substrates can be
 CC used to detect other putative abnormal APP processing events. They
 CC can also be used to investigate cellular post-translational
 CC modifications to APP in order to determine the potential influence
 CC on normal secretase and abnormal BAP 'clipping' activities.

XX Sequence 63 AA;

Query Match 100.0%; Score 47; DB 18; Length 63;
 Best Local Similarity 100.0%; Pred. No. 0.04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDA 10
 |||||||||
 DB 2 EISEVKMDA 11

Search completed: October 29, 2002, 10:26:42
 Job time : 25.1429 secs

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RESULT 15
AAW26391
ID AAW26391 standard; Peptide: 63 AA.
XX
AC AAW26391;
XX
DT 15-DEC-1997 (first entry)
XX
DE Amyloid precursor protein fragment APP-REP 751 (BAP E22Q).
XX
KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KW substrate; muten; secretase; Alzheimer's disease;
KW hereditary cerebral haemorrhage with amyloidosis; human.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Peptide 10..51
FT /label= BAP(E22Q)
FT /note= "beta-amyloid protein E22Q mutant"
FT Cleavage-site 25..26
FT /note= "secretase cleavage site"
FT Domain 38..61
FT /label= Transmembrane
XX
PN US5652092-A.
XX
PD 29-JUL-1997.
XX
PF 01-MAY-1992; 92US-0877675.
XX
PR 20-SEP-1993; 93US-0123659.
PR 01-MAY-1992; 92US-0877675.
PR 05-JUN-1995; 95US-0462859.
XX
PA (AMCY ) AMERICAN CYANAMID CO.
XX
PI Jacobsen JS, Vitek MP;
XX
DR MPI; 1997-392937/36.
XX
PT Screening for compounds which reduce beta-amyloid protein formation
PT - using cells which express a construct encoding a marker and an
PT amyloid precursor muten derived from APP isoforms
XX
PS Disclosure: Fig 5A; 8app; English.
XX
CC This peptide sequence shows the region of amyloid precursor protein
CC (APP) that includes a beta-amyloid protein (BAP) carrying a point
CC mutation (BAP E22Q) found in patients with hereditary cerebral
CC haemorrhage with amyloidosis of Dutch origin (HCHWA-D). In an
CC attempt to engineer an APP non-cleavable substrate for secretase,
CC an APP-reporter (APP-REP) protein that carries the E22Q mutation,
CC has been expressed in recombinant host cells. This resulted in the
CC secretion of an N-terminal fragment indistinguishable from that of
CC APP-REP 751 (see AAW26393-94). Non-cleavable APP substrates can be
CC used to detect other putative abnormal APP processing events. They
CC can also be used to investigate cellular post-translational
CC modifications to APP in order to determine the potential influence
CC on normal secretase and abnormal BAP 'clipping' activities.
CC
SQ Sequence 63 AA:

Query Match 100.0%; Score 47; DB 18; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEISEVKMDA 10
   |||||||||
Db 2 EEISEVKMDA 11

```

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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:36 : Search time 10.4286 Seconds
(without alignments)
92.140 Million cell updates/sec

Title: US-09-580-018-1
Perfect score: 47
Sequence: 1 EISEVKKMDA 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	82	2	P00438 Alzheimer's disease
2	47	100.0	695	1	A49795 Alzheimer's disease
3	47	100.0	695	2	A27485 Alzheimer's disease
4	47	100.0	695	2	S00550 Alzheimer's disease
5	47	100.0	770	1	ORH044 Alzheimer's disease
6	44	93.6	747	1	JH0773 Alzheimer's disease
7	37	78.7	146	2	C69136 hypothetical prote
8	34	72.3	62	2	T12832 hypothetical prote
9	33	70.2	33	2	S23094 beta-amyloid prote
10	33	70.2	57	2	E60045 Alzheimer's disease
11	33	70.2	57	2	E60045 Alzheimer's disease
12	33	70.2	57	2	E60045 Alzheimer's disease
13	33	70.2	57	2	E60045 Alzheimer's disease
14	33	70.2	57	2	E60045 Alzheimer's disease
15	33	70.2	57	2	E60045 Alzheimer's disease
16	33	70.2	64	2	T29319 hypothetical prote
17	33	70.2	95	2	A75133 hypothetical prote
18	33	70.2	96	2	D10175 hypothetical prote
19	33	70.2	370	2	T48633 hypothetical prote
20	33	70.2	389	2	G84245 NADH dehydrogenase
21	33	70.2	743	2	D84854 hypothetical prote
22	32	68.1	84	2	T27174 hypothetical prote
23	32	68.1	151	2	H90256 hypothetical prote
24	32	68.1	244	2	G96507 hypothetical prote
25	32	68.1	427	2	E5436 gamma-aminobutyric
26	32	68.1	488	2	JH0359 protein disulfide-
27	32	68.1	489	2	S68280 SWI protein homol
28	32	68.1	576	2	S27790
29	32	68.1	941	2	B96533 hypothetical prote

30	32	68.1	1121	2	G64103 exodeoxyribonuclea
31	32	68.1	1286	2	T02187 probable ABC trans
32	32	68.1	1637	2	T46438 hypothetical prote
33	31	66.0	105	2	PH1526 gamma-aminobutyric
34	31	66.0	140	2	T47308 hypothetical prote
35	31	66.0	143	2	T19218 hypothetical prote
36	31	66.0	178	2	C69206 hypothetical prote
37	31	66.0	195	2	A85070 hypothetical prote
38	31	66.0	244	2	E86471 unknown protein li
39	31	66.0	252	2	T05813 hypothetical prote
40	31	66.0	253	2	B84408 hypothetical prote
41	31	66.0	261	1	C64572 conserved hypothet
42	31	66.0	261	2	F71867 hypothetical prote
43	31	66.0	281	2	AH3629 taurine transport
44	31	66.0	288	2	T48268 DP-2 transcription
45	31	66.0	304	2	150721 syemnin - chicken

ALIGNMENTS

RESULT 1

P00438 Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: P00438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A>Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
A:Reference number: P00438; MUID:93075180
A:Accession: P00438
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:M83558; GB:M83657
R:Johnstone, E.M.; Chaney, M.O.; Morris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match

Best Local Similarity 100.0%; Score 47; DB 2; Length 82;
Pred. No. 0.017; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKKMDA 10
Db 9 EISEVKKMDA 18

RESULT 2

A49795 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlinsky, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A>Title: Homology of the amyloid beta protein precursor in monkey and human supports
A:Reference number: A49795; MUID:91273117
A:Accession: A49795
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>
A:Cross-references: GB:M58727; NID:9342062; PIDD:AAA36829.1; PID:9342063
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing

Query Match 100.0%; Score 47; DB 1; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEISEYKMDA 10
 |||||||
 Db 589 EEISEYKMDA 598

RESULT 3

A27485
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
 N:Alternate names: proteinase nexin II
 C:Species: Mus musculus (house mouse)
 C>Date: 31-Mar-1989 #sequence,revision 31-Mar-1989 #text_change 13-Aug-1999
 C:Accession: A27485; S19727; I49485
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precu
 A:Reference number: A27485; MUID:88106489
 A:Accession: A27485
 A:Molecule type: mRNA
 A:Residues: 1-695 <RAM>
 A:Cross-references: GB:M18373; NID:q191568; PIDN:AAA37139.1; PID:q309085
 A:Experimental source: Brain
 R:de Strooper, B.; van Leuven, F.; van den Berghe, H.
 Biochim. Biophys. Acta 1129, 141-143, 1991
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
 A:Reference number: S19727; MUID:92096458
 A:Accession: S19727
 A:Molecule type: mRNA
 A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
 A:Cross-references: EMBL:X59379
 R:Izum, R.; Yamada, T.; Yoshikata, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
 Gene 112, 189-195, 1992
 A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's
 A:Reference number: I49485; MUID:92209398
 A:Accession: I49485
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-19 <RES>
 A:Cross-references: GB:D10603; NID:q220328; PIDN:BA01456.1; PID:q220329
 C:Genetics:
 A:Map position: 16c3
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 100.0%; Score 47; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEISEYKMDA 10
 |||||||
 Db 589 EEISEYKMDA 598

RESULT 4

S00550
 Alzheimer's disease amyloid beta protein precursor - rat
 N:Alternate names: beta-A4 amyloid protein
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Jun-1989 #sequence,revision 30-Jun-1989 #text_change 13-Aug-1999
 C:Accession: S00550; A41245; A39820; S46251
 R:Shivers, B.D.; Hlilich, C.; Multhaupt, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
 EMBO J. 7, 1365-1370, 1988
 A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
 A:Reference number: S00550; MUID:88312583
 A:Accession: S00550
 A:Molecule type: mRNA
 A:Residues: 1-695 <SHI>
 A:Cross-references: EMBL:X07648; NID:q55616; PIDN:CAA30488.1; PID:q55617
 R:Schubert, D.; Schroeder, R.; Iacorbliere, M.; Saitoh, T.; Cole, G.
 Science 241, 223-226, 1988

A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan co
 A:Reference number: A41245; MUID:88264430
 A:Accession: A41245
 A:Molecule type: protein

A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
 A>Note: evidence for heparan sulfate attachment
 R:Hesse, L.; Benet, D.; Masters, C.L.; Multhaupt, G.
 FEBS Lett. 349, 109-116, 1994
 A:Title: The beta-A4 amyloid precursor protein binding to copper.

A:Reference number: S46251; MUID:94320627
 A:Contents: annotation; copper binding sites
 A>Note: rat peptides were isolated but not sequenced
 R:Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
 J. Biol. Chem. 266, 8464-8469, 1991

A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat b
 A:Reference number: A39820; MUID:91217087
 A:Accession: A39820

A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 18-32 <POT>

A:Experimental source: brain
 C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
 C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
 F:625-648/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 47; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEISEYKMDA 10
 |||||||
 Db 589 EEISEYKMDA 598

RESULT 5

Q0R004
 Alzheimer's disease amyloid beta protein precursor (validated) - human
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inh
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascu
 protein precursor splice form APP(770)
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-1987 #sequence,revision 28-Jul-1995 #text_change 15-Sep-2000
 C:Accession: S02260; S05194; A32277; A32260; A34486; I39452; I39451; I39453; I59562;
 4668; A28583; A29302; A60805; J00038; S06121; A60355; A59011; A38384; S29076; S38252;
 R:Lemstra, H.G.; Salbaum, J.M.; Multhaupt, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;
 Nucleic Acids Res. 17, 517-522, 1989
 A:Title: The PreA(65) precursor protein of Alzheimer's disease A4 amyloid is encode
 A:Reference number: S02260; MUID:89128427
 A:Accession: S02260
 A:Molecule type: DNA
 A:Residues: 1-288, 'V', 365-770 <LEM1>
 A:Cross-references: EMBL:X13466
 A>Note: alternative splice form APP(695)
 R:Lemstra, H.G.
 submitted to the EMBL Data Library, November 1988
 A:Reference number: S05194
 A:Accession: S05194
 A:Molecule type: DNA
 A:Residues: 1-14, 'W', 17-288, 'V', 365-770 <LEM2>
 A:Cross-references: EMBL:X13466; NID:q35398; PIDN:CAA31830.1; PID:q871360
 A>Note: alternative splice form APP(695)
 R:A Paul, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr
 A:Reference number: A32277; MUID:89165870
 A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <LAF>
 A:Cross-references: GB:M24546; GB:M24547; NID:q341202; PIDN:AA013654.1; PID:q516074
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila

A:Reference number: A33260; MUID:89392030
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 656-737 <J08>
 A:Cross-references: GB:M29270; NID:g178663; PIDN:AAA1768.1; PID:g178665
 R:Prelli, F.; Levy, E.; Van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
 A:Reference number: A35486; MUID:90321244
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRE1>
 A:Note: 693-Gln was found in DNA isolated from HCMA-D patients
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 87, 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A:Reference number: I39451; MUID:90236318
 A:Accession: I39452
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMF
 A:Molecule type: DNA
 A:Residues: 1-770 <Y051>
 A:Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
 A:Accession: I39451
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMF
 A:Molecule type: DNA
 A:Residues: 1-530, 'QMLMPVIPAFWEAKVGR' <Y052>
 A:Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168
 A:Accession: A59020
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMF
 A:Contents: annotation: erratum
 A:Note: revised physical map for reference I39451
 R:Levy, E.; Gorman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
 Science 248, 1122-1126, 1990
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
 A:Reference number: I39453; MUID:90260663
 A:Accession: I39453
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
 A:Note: a mutation with 693-Gln is presented
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
 A:Reference number: I59562; MUID:92022553
 A:Accession: I59562
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716, 'F', 718-737 <MUR>
 A:Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
 R:Kamino, K.; Orr, H.T.; Payami, H.; Wajsbman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukul, W.; Larson, E.; Heston, L.L.; Martin,
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
 A:Reference number: A44017; MUID:93035397
 A:Accession: A44017
 A:Molecule type: DNA
 A:Residues: 687-692, 'G', 694-718 <KAM1>
 A:Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
 A:Experimental source: familial Alzheimer disease family SB
 A:Note: sequence extracted from NCBI backbone (NCBI:P:115374)
 A:Accession: B44017
 A:Molecule type: DNA
 A:Residues: 687-718 <KAN2>
 A:Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
 A:Experimental source: familial Alzheimer disease family LT
 A:Note: sequence extracted from NCBI backbone (NCBI:P:115376)
 A:Note: this sequence has a silent mutation
 R:Kang, J.; Lemaitre, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
 Nature 335, 733-736, 1987
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
 A:Reference number: A03134; MUID:87144572

A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288, 'V', 365-770 <KAN>
 A:Cross-references: GB:Y00264; NID:g28525; PIDN:CAA6374.1; PID:g28526
 A:Note: alternative splice form APP(695)
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascula
 A:Reference number: A29030; MUID:87231971
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A:Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
 A:Note: the authors translated the codon GAG for residue 647 as Asp
 R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Safitoff, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A:Title: Characterization and chromosomal localization of a cDNA encoding brain amylo
 A:Reference number: A47584; MUID:87120328
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756, 'S', 758-770 <GOL>
 A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
 A:Experimental source: brain
 R:Ritani, R.E.; Gussella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van
 Science 235, 880-884, 1987
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near
 A:Reference number: A47585; MUID:87120329
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TRAN1>
 A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51664.1; PID:g177958
 R:DiVys, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaitre, H.G.; Kang, J.; Mue
 EMBO J. 7, 949-957, 1988
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 p
 A:Reference number: S02638; MUID:88296437
 A:Accession: S02638
 A:Molecule type: mRNA
 A:Residues: 672-678 <DIR>
 R:Ritani, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gussella, J.F.; N
 Nature 331, 528-530, 1988
 A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc
 A:Reference number: S00707; MUID:88122640
 A:Accession: S00707
 A:Molecule type: mRNA
 A:Residues: 286-344, 'I', 365-366 <TRAN2>
 A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g28812
 A:Experimental source: promyelocytic leukemia cell line HL60
 A:Note: alternative splice form APP(751)
 R:Ponte, P.; Gonzalez-Delital, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.;
 Nature 331, 525-527, 1988
 A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inh1
 A:Reference number: S00925; MUID:88122639
 A:Accession: S00925
 A:Molecule type: mRNA
 A:Residues: 1-344, 'I', 365-770 <PO2>
 A:Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
 A:Note: alternative splice form APP(771)
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhbl
 A:Reference number: A38944; MUID:88122642
 A:Accession: A38944
 A:Molecule type: mRNA
 A:Residues: 287-367 <KIT>
 A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g28811
 A:Experimental source: glioblastoma cell line
 A:Note: alternative splice form APP(770)
 R:Vittek, M.P.; Rasool, C.G.; de Sauvage, F.; Vittek, S.M.; Bartus, R.T.; Beer, B.; Ash
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre
 A:Reference number: A30320
 A:Accession: A30320
 A:Status: not compared with conceptual translation

A:Molecule type: mRNA
A:Residues: 384-788 'V', 365-770 <VIT1>
A:Accession: B30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288 'V', 365-770 <VIT2>
A:Accession: C30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease
A:Reference number: A31087; MUID:88124954
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <VIT>
A:Cross-references: GB:M18734; NID:g178572; PIDN:AA51726.1; PID:g178573
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 65
A:Note: The cited Genbank accession number, J03594, is not in release 101.0
R:Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther, K.
Query Match 100.0%; Score 47; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EISEVXMDA 10
|||||
DB 664 EISEVXMDA 673

RESULT 6
JH0773
A:Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 COKA
A:Cross-references: GB:S52417; NID:g263150; PIDN:AA824853.1; PID:g263151
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal kunitz-type proteinase inhibitor homology <BPI>
Query Match 93.6%; Score 44; DB 2; Length 747;
Best Local Similarity 90.0%; Pred. No. 0.83;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 EISEVXMDA 10
|||||
DB 641 EISEVXMDA 650

RESULT 7
C69136
A:hypothetical protein MTH286 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: C69136
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vitale, R.; Wang, Y.; Wlaczowski, J.; Gibson, R.; Jiwani, N.
Kl, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514
A:Accession: C69136

A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-146 <MTH>
A:Cross-references: GB:AE000814; GB:AE000666; NID:g2621334; PIDN:AA84792.1; PID:g262
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH286
A:Start codon: GTG
C:Superfamily: Methanobacterium thermoautotrophicum hypothetical protein MTH286
Query Match 78.7%; Score 37; DB 2; Length 146;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 EISEVXMD 9
|||||
DB 125 EELKVKMD 133

RESULT 8
T12832
A:hypothetical protein yonU - Bacillus subtilis phage SPBc2
C:Species: Bacillus subtilis phage SPBc2
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 15-Oct-1999
C:Accession: T12832; D69915
R:Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D.
submitted to the EMBL Data Library, August 1997
A:Description: The complete nucleotide sequence of the Bacillus subtilis spBc2 pro
A:Reference number: 217583
A:Accession: T12832
A>Status: preliminary; translated from GB/EMBL/DDAJ
A:Molecule type: DNA
A:Residues: 1-62 <LAU>
A:Cross-references: EMBL:AF020713; NID:g3025478; PID:g3025546; PIDN:AA13041.1
R:Kunet, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Calowell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmertson, P.T.; Ertlan, K.D.; Errington, J.; Fabre, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funo, S.; Galizzi, A.; Gal
leth, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holstappel, S.; Hosono, S.; Hullo, M
Koeber, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Ma
Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Paro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Roeha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanl
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasunori, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A:Reference number: A69580; MUID:98044033
A:Accession: D69915
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-62 <KUN>
A:Cross-references: GB:g99115; GB:AL009126; NID:g2634478; PIDN:CA14017.1; PID:el1835
A:Experimental source: strain 168
C:Genetics:
A:Gene: yonU
Query Match 72.3%; Score 34; DB 2; Length 62;
Best Local Similarity 77.8%; Pred. No. 5.6;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 EISEVXMD 9
|||||
DB 42 EELSKVKMD 50

RESULT 9
S23094
A:beta-amyloid protein precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996

C:Accession: S23094
 R:Kojima, S.; Omori, M.
 FEBS Lett. 304, 57-60, 1992
 A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
 A:Reference number: S23094; MUID:92316198
 A:Accession: S23094
 A:Molecule type: protein
 A:Residues: 1-33 <JO>
 A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

Query Match 70.2%; Score 33; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SEVKMDA 10
 Db 1 SEVKMDA 7

RESULT 10
 E60045

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
 C:Species: Ovis sp. (sheep)
 C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C:Accession: E60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; MUID:92017079
 A:Accession: E60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56130
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 70.2%; Score 33; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SEVKMDA 10
 Db 1 SEVKMDA 7

RESULT 11
 F60045

Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
 C:Accession: F60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; MUID:92017079
 A:Accession: F60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 70.2%; Score 33; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SEVKMDA 10
 Db 1 SEVKMDA 7

RESULT 12
 G60045

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
 C:Species: Cavia porcellus (guinea pig)
 C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C:Accession: G60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
 A:Reference number: A60045; MUID:92017079
 A:Accession: G60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56126
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 70.2%; Score 33; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SEVKMDA 10
 Db 1 SEVKMDA 7

RESULT 13
 D60045

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C:Accession: D60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
 A:Reference number: A60045; MUID:92017079
 A:Accession: D60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56124
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 70.2%; Score 33; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SEVKMDA 10
 Db 1 SEVKMDA 7

RESULT 14
 A60045

Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
 C:Species: Canis lupus familiaris (dog)
 C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C:Accession: A60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
 A:Reference number: A60045; MUID:92017079
 A:Accession: A60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56125
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 70.2%; Score 33; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SEVKMDA 10
 Db 1 SEVKMDA 7

Db 1 SEVKMDA 7

RESULT 15

B60045

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)

C:Species: ursus maritimus (polar bear)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C:Accession: B60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; MUID:92017079

A:Accession: B60045

A:Molecule type: mRNA

A:Residues: 1-57 <IOH>

A:Cross-references: EMBL:X56128; NID:92165; PIDN:CA39593.1; PID:92166

C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

70.2%; Score 33; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 8.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SEVKMDA 10
|||||||
Db 1 SEVKMDA 7Search completed: October 29, 2002, 10:30:57
Job time : 12.4286 secs

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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:36 ; Search time 5 Seconds
(without alignments)
77,439 Million cell updates/sec

Title: US-09-580-018-1
Perfect score: 47
Sequence: 1 EISEVKKMDA 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	47	100.0	751 1 A4_SAI5C	Q95241 salmrlr1 sci
2	47	100.0	770 1 A4_HUMAN	P05067 homo sapien
3	47	100.0	770 1 A4_MOUSE	P12023 mus musculu
4	47	100.0	770 1 A4_RAT	P08592 rattus norv
5	37	78.7	58 1 A4_CANFA	Q28280 canis fami
6	37	78.7	59 1 A4_BOVIN	Q28053 bos taurus
7	34	72.3	638 1 A4_MOUSE	Q31151 mus musculu
8	33	70.2	57 1 A4_PIG	Q29023 sus scrofa
9	33	70.2	57 1 A4_GRSMA	Q29149 ursus marit
10	33	70.2	58 1 A4_RABIT	Q28748 oryctolagus
11	33	70.2	58 1 A4_SHEEP	Q28757 ovis aries
12	32	68.1	230 1 T2E7_ECOLI	P50134 escherichia
13	32	68.1	332 1 MDHC_BETUV	Q9sm18 beta vulgar
14	32	68.1	488 1 GAB4_CHICK	P14045 gallus gall
15	32	68.1	575 1 SLP1_CAEEL	P14260 caenorhabdi
16	32	68.1	632 1 GAT_HUMAN	Q9un88 homo sapien
17	32	68.1	1121 1 EX5C_HAEM	P44954 haemophilus
18	31	66.0	227 1 G786_HUMAN	Q52520 homo sapien
19	31	66.0	451 1 HEMN_PAPDE	Q51676 paracoccus
20	31	66.0	479 1 ICE8_HUMAN	Q14790 h caspase-8
21	31	66.0	532 1 STE_LACDE	Q46083 lactobacilli
22	31	66.0	532 1 SAT1_HUMAN	P43007 homo sapien
23	31	66.0	613 1 SG2_BOVIN	P20616 bos taurus
24	31	66.0	630 1 SG4_BOVIN	Q9xt19 bos taurus
25	31	66.0	630 1 SG44_CAVPO	Q53899 cavia porce
26	31	66.0	630 1 SG44_HUMAN	P11645 homo sapien
27	31	66.0	630 1 SG44_MACMU	Q9myx0 macaca mula
28	31	66.0	630 1 SG44_MOUSE	Q60857 mus musculu
29	31	66.0	630 1 SG44_RAT	P31652 rattus norv
30	31	66.0	933 1 N1A_LEPMC	P36842 lepsochaer
31	31	66.0	1276 1 BMD_CLOBO	P19331 clostridium
32	31	66.0	1377 1 RPOC_BOBBU	O51339 borrelia bu
33	31	66.0	1682 1 MSP1_PLAF3	P19598 plasmodium

34	30	63.8	61 1 RL29_CAMJE	Q9plx9 campylobact
35	30	63.8	94 1 RL23_MYCCA	P10140 mycoplasma
36	30	63.8	104 1 YB04_MYCPA	P75565 mycoplasma
37	30	63.8	141 1 RL11_HELPY	P56037 helicobacte
38	30	63.8	257 1 YAI3_MYCPN	P75100 mycoplasma
39	30	63.8	263 1 ALF1_THERP	P58315 thermoprote
40	30	63.8	297 1 PHF7_MYCTU	O59566 mycobacteri
41	30	63.8	305 1 YOB8_BACSU	P45918 bacillus su
42	30	63.8	336 1 KC1B_BOVIN	P35507 bos taurus
43	30	63.8	432 1 OV71_ONCYO	P31732 onchocerca
44	30	63.8	442 1 SR54_METTH	O21736 methanobact
45	30	63.8	464 1 GAR3_RAT	P50373 rattus norv

ALIGNMENTS

```

RESULT 1
ID A4_SAI5C STANDARD: PRT; 751 AA.
AC Q95241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor [contains: Beta-
DE amyloid protein (Beta-Ap4) (A-beta)].
CN APP.
OS Salmrlr scireus (Common squirrel monkey).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Salmrlr.
CX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE: Liver, and Kidney.
RX MEDLINE=96108492; PubMed=8532114;
RA Levy E., Amorim A., Frangione B., Walker L.C.;
RT "beta-amyloid precursor protein gene in squirrel monkeys with
RT cerebral amyloid angiopathy.";
RL Neurobiol. Aging 16:805-808(1995).
CC -1- FUNCTION: FUNCTIONAL, NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC
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CC or send an email to license@sib-sib.ch)
CC
CC EMBL: S81024; RAD1437.1; -
CC HSP: P05067; IAPP
CC InterPro: IPR001868; A4_APP.
CC InterPro: IPR002223; Kunitz_BPTI.
CC Pfam: PF02177; A4_EXTRA; 1.
CC Pfam: PF00014; Kunitz_BPTI; 1.
CC PRINTS: PRO0203; AMYLOIDA.
CC PRINTS: PRO0759; BASICPTASE.
CC SMART: SM00006; A4_EXTRA; 1.
CC SMART: SM00131; KU; 1.
CC PROSITE: PS00319; A4_EXTRA; 1.
CC PROSITE: PS00320; A4_INTRA; 1.
CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.
CC PROSITE: PS02779; BPTI_KUNITZ_2; 1.

```

KM Glycoprotein: Amyloid; Neurone; Transmembrane; Alternative splicing;
 KW Signal: Serine protease inhibitor.
 FT CHAIN 1 17 BY SIMILARITY.
 FT CHAIN 18 751 A4 PROTEIN.
 FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 681 704 POTENTIAL.
 FT DOMAIN 705 751 CYTOSOLASMIC (POTENTIAL).
 FT DOMAIN 287 345 BPT/UNIT-1 INHIBITOR.
 FT SITE 740 743 CATHRIN-BINDING (BY SIMILARITY).
 FT ACT_SITE 301 302 REACTIVE BOND.
 FT DISULFID 251 341 BY SIMILARITY.
 FT DISULFID 300 324 BY SIMILARITY.
 FT DISULFID 316 337 BY SIMILARITY.
 FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).
 SQ SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;
 Query Match 100.0%; Score 47; DB 1; Length 751;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEISEVAKMDA 10
 DB 645 EEISEVAKMDA 654
 RESULT 2
 A4_HUMAN STANDARD; PRT; 770 AA.
 ID A4_HUMAN
 AC P05067; P09000; Q16011;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II) (P4-II) (APP1) [contains: Beta-amyloid protein (beta-APP) (A-beta)].
 OS Homo sapiens (Human).
 OC Amino acids; Human.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain:
 RX MEDLINE-87144572; PubMed-2881207;
 RA Kang J., Lemaitre H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grieschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor";
 RL Nature 325:733-736(1987).
 RN 12
 RP SEQUENCE FROM N.A.
 RX MEDLINE-8812639; PubMed-2893289;
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine protease inhibitors";
 RL Nature 331:525-527(1988).
 RN 13
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89128427; PubMed-2783775;
 RA Lemaitre H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The p36A(693) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons";
 RL Nucleic Acids Res. 17:517-522(1989).
 RN 14
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97263807; PubMed-9108154;
 RA Hattori M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for

RT sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN 15
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
 RX MEDLINE-88122640; PubMed-2893290;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L., Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 RN 16
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE-88122641; PubMed-2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory activity.";
 RL Nature 331:530-532(1988).
 RN 17
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
 RX MEDLINE-87231971; PubMed-3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN 18
 RP SEQUENCE OF 507-770 FROM N.A.
 RX MEDLINE-88124954; PubMed-2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E., Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease brain: coding and noncoding regions of the fetal precursor mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN 19
 RP SEQUENCE OF 672-681.
 RX MEDLINE-88035004; PubMed-3312495;
 RA Farridge W.W., Vinters H.V., Yang J., Eisenberg J., Choi T.B., Tourtelotte W.W., Hoeber V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition and partial sequence of a 4,200-dalton peptide isolated from cortical microvessels.";
 RL J. Neurochem. 49:1394-1401(1987).
 RN 110
 RP SEQUENCE OF 739-770 FROM N.A.
 RX MEDLINE-90236318; PubMed-2110105;
 RA Yoshikai S., I., Sakaki H., Doh-ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor gene.";
 RL Gene 87:257-263(1990).
 RN 111
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE-Liver:
 RX MEDLINE-89016647; PubMed-3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP) encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN 112
 RP SEQUENCE OF 18-50.
 RX MEDLINE-87250462; PubMed-3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J Biol. Chem. 262:8508-8514(1987).
 RN 113
 RP IDENTITY OF APP WITH NEXIN-II.
 RX MEDLINE-89384866; PubMed-2506449;
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I., Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F., Sinha S.;
 RT "The secreted form of the Alzheimer's amyloid precursor protein with the Kunitz domain is protease nexin-II.";
 RL Nature 341:144-147(1989).
 RN 114

RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RA MEDLINE=90211252; PubMed=1969731;
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
 RT Protease-specificity of Kunitz inhibitor domain of Alzheimer's
 RT disease amyloid protein precursor.";
 RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
 RN [15]
 RP COMPLEX WITH G(O).
 RX MEDLINE=93188965; PubMed=8446172;
 RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
 RA Murayama Y., Ogata E.;
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 RT protein G(O)." ;
 RL Nature 362:75-79(1993).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 287-344.
 RX MEDLINE=99215582; PubMed=10201399;
 RA Rossjohn J., Cappai R., Fell S.C., Henry A., Mckinstrey W.J.,
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RT Crystal structure of the N-terminal, growth factor-like domain of
 RT Alzheimer amyloid precursor protein." ;
 RL Nat. Struct. Biol. 6:327-331(1999).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
 RX MEDLINE=91104913; PubMed=1125487;
 RA Hyres T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kosiakof A.A.;
 RT "X-ray crystal structure of the protease inhibitor domain of
 RT Alzheimer's amyloid beta-protein precursor." ;
 RL Biochemistry 29:10018-10022(1990).
 RN [18]
 RP STRUCTURE BY NMR OF 289-344.
 RX MEDLINE=92031488; PubMed=1718421;
 RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,
 RA Kamatsek M.S., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
 RA Tamburini P.P.;
 RT Sequential NMR resonance assignment and structure determination of
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
 RT precursor protein." ;
 RL Biochemistry 30:10467-10478(1991).
 RN [19]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=94281210; PubMed=7516706;
 RA Talatous J., Marciniowski K.J., Klopman G., Zagorski M.G.;
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide." ;
 RL Biochemistry 33:7788-7796(1994).
 RN [20]
 RP STRUCTURE BY NMR OF 696-706.
 RX MEDLINE=97128622; PubMed=8973180;
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
 RT membrane-mimicking environment." ;
 RL Biochemistry 35:16094-16104(1996).
 RN [21]
 RP STRUCTURE BY NMR OF 672-711.
 RX MEDLINE=96359783; PubMed=9693002;
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscelle
 RT environment. Is the membrane-spanning domain where we think it is?" ;
 RL Biochemistry 37:11064-11077(1998).
 RN [22]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=20400066; PubMed=10940222;
 RA Poulsen S.-A., Watson A.A., Craik D.J.;
 RT "Solution structures in aqueous SDS micelles of two amyloid beta
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
 RT site." ;
 RL J. Struct. Biol. 130:142-152(2000).
 RN [23]
 RP STRUCTURE BY NMR OF 681-706.
 RX MEDLINE=20400065; PubMed=10940221;
 RA Zhang S., Iwata K., Lachemann M.J., Peng J.W., Li S., Stinson E.R.,
 RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;

RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in
 RT water." ;
 RL J. Struct. Biol. 130:130-141(2000).
 RN [24]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
 RX MEDLINE=88296437; PubMed=2900137;
 RA Dykx T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
 RT "Identification, transmembrane orientation and biogenesis of the
 RT amyloid A4 precursor of Alzheimer's disease." ;
 QY 1 PEISEVKMDA 10
 DB 664 EISEVKMDA 673
 QY 1 PEISEVKMDA 10
 DB 664 EISEVKMDA 673
 Query Match 100.0%; Score 47; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 3
 A4_MOUSE STANDARD: PRT; 770 AA.
 ID A4_MOUSE
 AC P12023;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog precursor
 DE (Amyloidogenic glycoprotein) (AG).
 GN APP
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC STRAIN-BALB/C; TISSUE-Brain;
 RX MEDLINE=92096458; PubMed=1756177;
 RA de Strooper B., van Leuven F., van den Berghe H.;
 RT "The amyloid beta protein precursor or protease nexin II from mouse
 RT is closer related to its human homolog than previously reported." ;
 RL Biochim. Biophys. Acta 1129:141-143(1991).
 RN [2]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=88106489; PubMed=3322280;
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sasaki Y.;
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 RT protein precursor." ;
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
 RN [3]
 RP REVISIONS.
 RA Yamada T.;
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN-CD-1; TISSUE-Placenta;
 RX MEDLINE=89345111; PubMed=2569710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of Mus domestica." ;
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [5]
 RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE=92209998; PubMed=1555768;
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
 RA Sakai Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse." ;
 RL Gene 112:189-195(1992).
 RN [6]
 RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE-Brain, and Kidney;

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RX MEDLINE-89149813; PubMed-2493250;
RA Yamada T., Sasaki H., Dohura K., Ooto I., Sakaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RT for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor."
RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY AAA(751) IS
CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
CC LIVER.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NEXT MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: X59379; -; NOT ANNOTATED_CDS.
DR EMBL: M18373; AAA7339.1; -
DR EMBL: X15210; CAA33280.1; -
DR EMBL: D10603; BAA01456.1; -
DR EMBL: M24397; AAA39929.1; -
DR PIR: A27485; A27485.
DR PIR: S04855; S04855.
DR PIR: S19727; S19727.
DR HSSP: P05067; IQCM.
DR MGD: MGI:88059; APP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurope; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT SIGNAL 17
FT CHAIN 18 770
FT FT 18 770
FT TRANSHEM 18 599
FT DOMAIN 700 723
FT DOMAIN 724 770
FT DOMAIN 673 715
FT DOMAIN 287 345
FT SITE 759 762
FT DISULFID 291 341
FT DISULFID 300 324
FT DISULFID 316 337
FT CARBOHYD 542 542
FT CARBOHYD 571 571
FT VARSPLIC 289 364
FT VARSPLIC 346 380
FT SEQUENCE 770 AA: 86752 MW: 26C5D0E896CA7A CAC64;
Query Match 100.0%; Score 47; DB 1; Length 770;

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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEISEVKMDA 10
Db 664 EEISEVKMDA 673
RESULT 4
AC A4_RAT STANDARD; PRT; 770 AA.
AC P08592;
DT 01-AUG-1988 (Rel. 08. Created)
DT 01-DEC-1992 (Rel. 24. Last sequence update)
DT 16-OCT-2001 (Rel. 40. Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (Ag).
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RP TISSUE=Brain;
RX MEDLINE-88312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact."
RL EMBO J. 7:1365-1370(1988).
RP SEQUENCE OF 289-364 FROM N.A.
RP TISSUE=Liver;
RX MEDLINE-89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4."
RL Nucleic Acids Res. 17:2130-2130(1989).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NEXT MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC -----
DR EMBL: X07648; CAA30488.1; -
DR EMBL: X14066; CAA32229.1; -
DR PIR: S00550; S00550.
DR PIR: S03607; S03607.
DR HSSP: P05067; IAAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.

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DR PROSITE: PS00280; BPTL_KUNITZ_1;
DR PROSITE: PS00279; BPTL_KUNITZ_2; 1.
KM Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 770
FT DOMAIN 18 699
FT TRANSSEM 700 723
FT DOMAIN 724 770
FT DOMAIN 673 715
FT DOMAIN 287 345
FT SITE 739 762
FT DISULFID 291 341
FT DISULFID 300 324
FT DISULFID 316 337
FT CARBOHYD 542 542
FT CARBOHYD 571 571
FT VARSPIC 289 289
FT VARSPIC 290 364
SQ SEQUENCE 770 AA; 86704 MW; C26C9D6BBD292A7 CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 770;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EISEVKMDA 10
Db 664 EISEVKMDA 673

RESULT 5
A4 CANFA STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-Ap) (A-beta)] (Fragment).
GN App.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA MEDLINE=92017079; PubMed=1656157;
RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC GAO (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL: X56125; CAA39590.1; -.
CC HSSP: P05067; 1BA4.
CC InterPro: IPR001868; A4_APP.
CC PROSITE: PS00319; A4_EXTRA; PARTIAL.
CC PROSITE: PS00320; A4_INTRA; PARTIAL.
CC PROSITE: PS00320; A4_INTRA; PARTIAL.

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KM Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 7 49
FT DOMAIN <1 34
FT TRANSSEM 35 58
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match
Best Local Similarity 78.7%; Score 37; DB 1; Length 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ISEVKMDA 10
Db 1 ISEVKMDA 8

RESULT 6
A4 BOVIN STANDARD; PRT; 59 AA.
ID A4_BOVIN
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-Ap) (A-beta)] (Fragment).
GN App.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=92017079; PubMed=1656157;
RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC GAO (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL: X56124; CAA39589.1; -.
CC HSSP: X56126; CAA39591.1; -.
CC HSSP: P05067; 1BA4.
CC InterPro: IPR001868; A4_APP.
CC PROSITE: PS00319; A4_EXTRA; PARTIAL.
CC PROSITE: PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 1
FT DOMAIN 7 49
FT TRANSSEM 35 58
FT DOMAIN <1 34
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match
Best Local Similarity 78.7%; Score 37; DB 1; Length 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      3 ISEYKMDA 10
        |||||
DB      1 ISEYKMDA 8

RESULT 7
GAAT_MOUSE STANDARD: PRT: 638 AA.
ID GAAT_MOUSE STANDARD: PRT: 638 AA.
AC Q9JLF1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gamma-aminobutyric-acid receptor theta subunit precursor (GABA(A)
DE receptor).
GN GABRO.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-2026167; PubMed-10804200;
RX Sirkkonen S.T., Hanna M.C., Kirkness E.F., Korpi E.R.;
RZ "GABAA receptor epsilon and theta subunits display unusual structural
RT variation between species and are enriched in the rat locus
RL ceruleus."
RT J. Neurosci. 20:3588-3595(2000).
CC -1- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC CHANNEL.
CC -1- SUBUNIT: GENERALLY PENTAMERIC. THIS SUBUNIT COASSEMBLES WITH
CC ALPHA-2, BETA-1, AND GAMMA-1.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC -----
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CC -----
DR EMBL: AF189260; AAF70381.1; -
DR MCD: MG1:1888498; Gabrg.
DR InterPro: IPR001175; Neur_chan.
DR Pfam: PF02931; Neur_chan_LBD; 1.
DR Pfam: PF02932; Neur_chan_memb; 1.
DR PRINTS: PS00252; NRIONCHANNEL.
DR PROSITE: PS00236; NEURORTR_ION_CHANNEL; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; signal;
KW Multigene family; Transmembrane.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 638 GAMMA-AMINOBUTYRIC-ACID RECEPTOR THETA
FT SUBUNIT.
FT DOMAIN 22 267 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 268 288 POTENTIAL.
FT TRANSMEM 326 346 POTENTIAL.
FT TRANSMEM 618 638 POTENTIAL.
FT DISULFID 183 197 BY SIMILARITY.
FT CARBOHYD 127 127 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 638 AA: 72799 MW: 452440295BFA3 CRC64.

Query Match 72.3%; Score 34; DB 1; Length 638;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY      1 EEISEVKMD 9
        |::|::|
DB      95 E0ISEINMD 103

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RESULT 8
A4_PIG STANDARD: PRT: 57 AA.
ID A4_PIG STANDARD: PRT: 57 AA.
AC Q29023;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-ApP) (A-beta)] (Fragment).
GN APP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE-92017079; PubMed-1656157;
RA Johnstone E.M., Chaney M.O., Morris F.H., Pascual R., Little S.P.;
RZ "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: X56127; CAA39592.1; -
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57 57
SQ SEQUENCE 57 AA: 6172 MW: 84209D88EBA82DFA CRC64.

Query Match 70.2%; Score 33; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      4 SEYKMDA 10
        |||||
DB      1 SEYKMDA 7

RESULT 9
A4_URSMA STANDARD: PRT: 57 AA.
ID A4_URSMA STANDARD: PRT: 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (beta-ApP) (A-beta)] (Fragment).
GN APP.
OS Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.

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OX  NCBI_TaxID=29073;
RN  (1)
RP  SEQUENCE FROM N.A.
RC  TISSUE=Brain;
RX  MEDLINE=92017079; PubMed=1656157;
RA  Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT  "Conservation of the sequence of the Alzheimer's disease amyloid
RL  peptide in dog, polar bear and five other mammals by cross-species
RT  polymerase chain reaction analysis.";
RL  Brain Res. Mol. Brain Res. 10:299-305(1991).
CC  -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC  INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC  G(O) (BY SIMILARITY).
CC  -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC  or send an email to license@isb-sib.ch).
-----
DR  EMBL: X56128; CAA39593.1; -.
DR  HSSP: P05067; IAML.
DR  InterPro: IPR001868; A4_APP.
DR  PROSITE: PS00319; A4_EXTRA: PARTIAL.
DR  PROSITE: PS00320; A4_INTRA: PARTIAL.
KW  Glycoprotein; Amyloid; Neurone; Transmembrane.
FT  NON_TER 1
FT  CHAIN 1
FT  DOMAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT  TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).
FT  NON_TER 57 57 POTENTIAL.
SQ  SEQUENCE 57 AA; 6172 MW; 84209D88EBA82D CRC64;

Query Match 70.2%; Score 33; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SEVKMDA 10
Db 1 SEVKMDA 7

RESULT 10
A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
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-!- SUBCELLULAR LOCATION: Type I membrane protein.
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CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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DR EMBL: X56129; CAA39594.1; -.
DR HSSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA: PARTIAL.
DR PROSITE: PS00320; A4_INTRA: PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 1
FT DOMAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 58 58 POTENTIAL.
FT NON_TER 58 58 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 70.2%; Score 33; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SEVKMDA 10
Db 1 SEVKMDA 7

RESULT 11
A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
-----
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-----
DR EMBL: X56130; CAA39595.1; -.
DR HSSP: P05067; IAML.
-----
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DR InterPro: IPR001868; A4_APP.
 DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE: PS00320; A4_INTRA; PARTIAL.
 KM Glycoprotein; Amyloid; Neurone; Transmembrane.
 FT NON_TER 1 1
 FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 34 57 POTENTIAL.
 FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
 FT NON_TER 58 58
 SQ SEQUENCE 58 AA; 6300 MW; F43420988EBA82D CRC64;
 Query Match 70.2%; Score 33; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SEVKMDA 10
 |||||
 DB 1 SEVKMDA 7

RESULT 12
 T2E7_ECOLI STANDARD; PRT; 230 AA.
 AC P50194;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Type II restriction enzyme Eco47I (EC 3.1.21.4) (Eco47I)
 DE (R.Eco47I).
 GN Eco47IR.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OC NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=REL47;
 RX MEDLINE=95331599; PubMed=7607524;
 RA Stakkevicius K., Povilionis P., Lubys A., Menkevicius S.,
 RA Janulaitis A.;
 RT Cloning and characterization of the unusual restriction-modification
 RT system comprising two restriction endonucleases and one
 RT methyltransferase.";
 RL Gene 157:49-53(1995).
 CC -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE GGNCC AND
 CC CLEAVES AFTER G-1.
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
 CC specific double-stranded fragments with terminal 5'-phosphates.
 CC -1- SIMILARITY: TO R.SIN1.
 CC -----
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 CC -----
 DR EMBL: X82105; CAA57630.1; -.
 DR REBASE: 930; Eco47I.
 KM Hydrolyase; Endonuclease; Nuclease; Restriction system.
 SQ SEQUENCE 230 AA; 26864 MW; AA3621FF506DFB11 CRC64;

Query Match 68.1%; Score 32; DB 1; Length 230;
 Best Local Similarity 60.0%; Pred. No. 33;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EISEVKMDA 10
 ||::: ||||
 DB 12 EELAKOKMDA 21

RESULT 13
 MDHC_BETUV STANDARD; PRT; 332 AA.
 ID MDHC_BETUV
 AC Q9SMD8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Malate dehydrogenase, cytoplasmic (EC 1.1.1.37).
 GN NRI.
 OS Beta vulgaris (Sugar beet).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllales; Chenopodiaceae; Beta.
 OX NCBI_TaxID=3555;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RA Juergensen K., Buck F., Lange S., Kleine M., Grundler F.M.W.;
 RT "A Beta vulgaris cDNA coding for a putative cytoplasmatic malate
 RT dehydrogenase.";
 RL (In) Plant Gene Register PGR00-023.
 CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY, MDH SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: AJ251083; CAB61618.1; -.
 DR HSSP: P11708; 4MDH.
 DR InterPro: IPR001252; MDH_actsite.
 DR InterPro: IPR001236; Idh.
 DR Pfam: PF00056; Idh; 1.
 DR Pfam: PF00866; Idh_C; 1.
 DR ProDom: PD003052; MDH_actsite; 1.
 DR PROSITE: PS00068; MDH; 1.
 DR Oxidoreductase; Tricarboxylic acid cycle; NAD.
 KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
 FT ACT_SITE 160 160 PROTON-RELAY (BY SIMILARITY).
 FT BINDING 163 163 SUBSTRATE CARBOXYL GROUP (BY SIMILARITY).
 FT ACT_SITE 188 188 PROTON-RELAY (BY SIMILARITY).
 FT ACT_SITE 188 188
 SQ SEQUENCE 332 AA; 35434 MW; 2B9E6495EFCDD12A CRC64;
 Query Match 68.1%; Score 32; DB 1; Length 332;
 Best Local Similarity 60.0%; Pred. No. 49;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EISEVKMDA 10
 ||:| ||||
 DB 306 DEVSRKMDA 315

RESULT 14
 GABA_CHICK STANDARD; PRT; 488 AA.
 ID GABA_CHICK
 AC P24045;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUL-1992 (Rel. 38, Last annotation update)
 DE Gamma-aminobutyric-acid receptor beta-4 subunit precursor (GABA(A)
 DE receptor).
 GN GABRB4.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.

```

RC TISSUE=Brain;
RX MEDLINE=91162222; PubMed=1848280;
RA Bateson A.N., Lasham A., Darlison M.G.;
RT Gamma-aminobutyric acid A receptor heterogeneity is increased by
RL alternative splicing of a novel beta-subunit gene transcript.";
RL J. Neurochem. 56:1437-1440(1991).
CC -1- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC CHANNEL.
CC -1- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: BETA-4 AND BETA-4' (SHOWN HERE);
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC -----
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CC -----
DR EMBL: X56647; CA39969.1; -.
DR EMBL: X56648; CA39970.1; ALT_SEQ.
DR PIR: JH0360; JH0360.
DR PIR: JH0359; JH0359.
DR InterPro: IPR000188; GABA_A_receptor.
DR InterPro: IPR001175; Neur_channel.
DR Pfam: PF02931; Neur_chan_LBD; 1.
DR Pfam: PF02932; Neur_chan_membr; 1.
DR PRINTS: PR00252; NRIONCHANNEL.
DR PROSITE: PS00236; NEUROTRION_CHANNEL; 1.
DR Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KM Multigene family; Transmembrane; Alternative splicing.
FT SIGNAL 1 25
FT CHAIN 26 488
FT DOMAIN 26 244
FT TRANSMEM 245 266
FT TRANSMEM 271 292
FT TRANSMEM 304 326
FT DOMAIN 327 465
FT TRANSMEM 466 487
FT CARBOHYD 32 32
FT CARBOHYD 104 104
FT CARBOHYD 173 173
FT CARBOHYD 195 195
FT DISULFID 160 174
FT VARSPIC 361 364
SQ SEQUENCE 488 AA; 56068 MW; 164A75314BDB2C12 CRC64;

Query Match 68.1%; Score 32; DB 1; Length 488;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EISEVKMD 9
DB 72 DQISEVND 80

RESULT 15
SLIP_CAEEL STANDARD; PRT; 575 AA.
AC P34260;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein slip-1.
GN SLP-1 OR B0303.9.
OS Caenorhabditis elegans.

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OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=92168156; PubMed=1538779;
RA Sulston J., Du Z., Thomas K., Wilson R., Hillier L., Staden R.,
RA Halloran N., Green P., Thierry-Mieg J., Qin L., Dear S., Coulson A.,
RA Craxton M., Durbin R.K., Berks M., Metzstein M., Hawkins T.,
RA Alnouch R., Waterston R.;
RT "The C. elegans genome sequencing project: a beginning.";
RL Nature 356:37-41(1992).
CC -1- SIMILARITY: TO YEAST SLP1.
CC -----
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CC -----
DR EMBL: M77697; AAA27901.1; -.
DR PIR: S27790; S27790.
DR WormPep: B0303.9; CE00539.
DR InterPro: IPR001619; Sec1.
DR Pfam: PF00995; Sec1; 1.
KM Protein transport.
SQ SEQUENCE 575 AA; 64814 MW; 7FC4A06D896C9AAB CRC64;

Query Match 68.1%; Score 32; DB 1; Length 575;
Best Local Similarity 66.7%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EISEVKMD 9
DB 476 EFSEAKLD 484

```

Search completed: October 29, 2002, 10:27:24
Job time : 7 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:11 : Search time 18 seconds

(without alignments)
96.108 Million cell updates/sec

Title: US-09-580-018-1

Perfect score: 47

Sequence: 1 EISEVKMDA 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	79	11	035463
2	47	100.0	82	4	P78438
3	47	100.0	82	4	016014
4	47	100.0	82	4	016019
5	47	100.0	82	4	016020
6	47	100.0	607	11	099K32
7	47	100.0	695	6	Q95KN7
8	47	100.0	695	11	P97487
9	47	100.0	695	11	060496
10	47	100.0	770	6	Q9TUI0
11	46	97.9	534	13	Q93296
12	46	97.9	569	13	Q9PVL1
13	46	97.9	695	13	Q9DG38
14	46	97.9	751	13	Q9DCJ7
15	44	93.6	693	13	Q98SG0
16	44	93.6	695	13	Q98SF9

17	44	93.6	747	13	Q91963	Q91963 xenopus. ap
18	37	78.7	146	17	Q26386	Q26386 methanother
19	37	78.7	857	15	Q66956	Q66956 feline immu
20	35	74.5	1103	10	Q9LYX3	Q9LYX3 arabidopsis
21	34	72.3	62	9	Q64081	Q64081 bacterioph
22	34	72.3	62	16	Q31940	Q31940 bacillus su
23	34	72.3	141	2	Q44749	Q44749 borrelia bu
24	34	72.3	141	2	Q44784	Q44784 borrelia bu
25	34	72.3	141	2	Q9R3H3	Q9R3H3 borrelia bu
26	34	72.3	141	2	Q9R9B8	Q9R9B8 borrelia bu
27	34	72.3	141	2	Q9S0J3	Q9S0J3 borrelia bu
28	34	72.3	141	2	Q9S0A9	Q9S0A9 borrelia bu
29	34	72.3	141	2	Q9S037	Q9S037 borrelia bu
30	34	72.3	141	2	Q9RZY5	Q9RZY5 borrelia bu
31	34	72.3	141	2	Q86117	Q86117 borrelia bu
32	34	72.3	141	2	Q07496	Q07496 borrelia bu
33	34	72.3	141	2	Q44779	Q44779 borrelia bu
34	34	72.3	141	2	Q44788	Q44788 borrelia bu
35	34	72.3	545	10	Q9FE41	Q9FE41 arabidopsis
36	34	72.3	635	11	Q912M7	Q912M7 rattus norv
37	34	72.3	869	5	Q9V610	Q9V610 drosophila
38	33	70.2	64	5	P91000	P91000 caenorhabdi
39	33	70.2	95	17	Q9V0C6	Q9V0C6 pyrococcus
40	33	70.2	96	17	Q74008	Q74008 pyrococcus
41	33	70.2	233	4	Q95999	Q95999 homo sapien
42	33	70.2	233	11	Q920H7	Q920H7 mus musculu
43	33	70.2	233	11	Q9QYN5	Q9QYN5 rattus norv
44	33	70.2	370	10	Q9LYK0	Q9LYK0 arabidopsis
45	33	70.2	389	17	Q9HR27	Q9HR27 halobacteri

ALIGNMENTS

RESULT 1						
ID	035463	PRELIMINARY;	PRT;	79	AA.	
AC	035463:					
DT	01-JAN-1998 (TREMBLrel. 05, Created)					
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)					
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)					
DE	ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).					
GN	BETA APP.					
OS	Cricetulus griseus (Chinese hamster).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;					
OC	Cricetulus.					
OX	NCBI_TaxID=10029;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Sambamurti K., Pinnix I., Gandhi S.;					
RL	Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.					
DR	EMBL; AF030413; AAB86608.1; .					
DR	HSSP; P05067; 1BA4.					
FT	NON_TER	1				
FT	NON_TER	79	79			
SEQ	SEQUENCE	79	AA;	8538	MM;	37F2C6C3BF3F597 CRC64;
Query Match				100.0%;	Score 47;	DB 11;
Best Local Similarity				100.0%;	Pred. No. 0.057;	Length 79;
Matches	10;	Conservative	0;	Mismatches	0;	Indels
						Gaps 0;
QY	1 EISEVKMDA 10					
DB	13 EISEVKMDA 22					
RESULT 2						
ID	P78438	PRELIMINARY;	PRT;	82	AA.	
AC	P78438:					
DT	01-MAY-1997 (TREMBLrel. 03, Created)					
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)					

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DT 01-MAR-2001 (TREMBLREL. 16, Last annotation update)
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).
GN APP.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [2]
RP SEQUENCE OF 19-48 FROM N.A.
RX MEDLINE=87120329; PubMed=2949367;
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Nave R.L.;
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
RT linkage near the Alzheimer locus.";
RL Science 235:880-884(1987).
RN [3]
RP SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE=93035397; PubMed=1415269;
RA Kamino K., Orr H.T., Payaml H., Wajzman E.M., Alonso M.E., Pulst S.M.,
RA Anderson L., O'dahl S., Nemens E., White J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease
RT kindreds for the APP gene region.";
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL: M29270; AAAS1768.1; -
DR EMBL: M29269; AAAS1768.1; JOINED.
DR EMBL: M15532; AAAS1564.1; -
DR EMBL: S45136; AAB23646.1; -
DR HSSP: P05067; IBA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKKMDA 10
DB 9 EISEVKKMDA 18

RESULT 3
ID Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (TREMBLREL. 01, Created)
DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S60721; AAB26263.2; -
DR HSSP: P05067; IBA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

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Query Match
Best Local Similarity 100.0%; Score 47; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKKMDA 10
DB 10 EISEVKKMDA 19

RESULT 4
ID Q16019 PRELIMINARY; PRT; 82 AA.
AC Q16019;
DT 01-NOV-1996 (TREMBLREL. 01, Created)
DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S61380; AAB26264.2; -
DR HSSP: P05067; IBA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKKMDA 10
DB 10 EISEVKKMDA 19

RESULT 5
ID Q16020 PRELIMINARY; PRT; 82 AA.
AC Q16020;
DT 01-NOV-1996 (TREMBLREL. 01, Created)
DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S61383; AAB26265.2; -
DR HSSP: P05067; IBA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 EISEVXKMDA 10
 |||||||
 Db 10 EISEVXKMDA 19

RESULT 6
 099K32 PRELIMINARY; PRT; 607 AA.

AC 099K32: 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HYPOTHETICAL 68.4 KDA PROTEIN (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MAMMARY TUMOR. MAP-TGF ALPHA MODEL. 7 MONTHS OLD. GROSS
 RC TISSUE;
 RA Strausberg R.
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; EC005490; AAH05490.1; -.
 DR HSSP; P05067; 1AAP.
 DR InterPro; IPR001868; A4_APP.
 DR Pfam; PF002223; Kunitz_BPTI.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00280; A4_INTRA; 1.
 DR PROSITE; PS00320; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Hypothetical protein, Serine protease inhibitor.
 FT NON_TER
 FT SEQUENCE 607 AA; 68391 MW; BFP02214CBA7D172 CRC64;
 SQ

Query Match 100.0%; Score 47; DB 11; Length 607;
 Best Local Similarity 100.0%; Pred. No. 0.46;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVXKMDA 10
 |||||||
 Db 501 EISEVXKMDA 510

RESULT 7
 095KN7 PRELIMINARY; PRT; 695 AA.

AC 095KN7: 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE AMYLOID B-PROTEIN PRECURSOR.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CEREBELLUM;
 RX MEDLINE=91273117; PubMed=1905108;
 RA Podlinsky M.B., Tolan D.R., Selkoe D.J.;
 RT "Homology of the amyloid beta protein precursor in monkey and human
 RT supports a primate model for beta amyloidosis in Alzheimer's
 RT disease".
 RL Am. J. Pathol. 138:1423-1435(1991).
 DR EMBL; M58727; AAA36829.1; -.
 FT SIGNAL 1
 FT POTENTIAL. 17

FT CHAIN 597 636 POTENTIAL.
 SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match 100.0%; Score 47; DB 6; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVXKMDA 10
 |||||||
 Db 589 EISEVXKMDA 598

RESULT 8
 P97487 PRELIMINARY; PRT; 695 AA.

AC P97487: 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HIPPOCAMPAL AMYLOID PROTEIN.
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SAMP8; TISSUE=HIPPOCAMPUS;
 RA Flood J.F., Kumar V.B., Sasser T., Word I., Morley J.E.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 581-662 FROM N.A.
 RC STRAIN=129SV;
 RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capechli M.,
 RA Loring J.F., Goate A.M.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U84012; AAB41502.1; -.
 DR EMBL; U82624; AAB40919.1; -.
 DR HSSP; P05067; 1MWP.
 DR MCD; MGI:88059; APP.
 DR InterPro; IPR001868; A4_APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78414 MW; 9A5FBEE2ED261236E CRC64;
 SQ

Query Match 100.0%; Score 47; DB 11; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVXKMDA 10
 |||||||
 Db 589 EISEVXKMDA 598

RESULT 9
 060496 PRELIMINARY; PRT; 695 AA.

AC 060496: 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PUTATIVE AMYLOID PRECURSOR PROTEIN.
 OS Cavia sp. Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10143;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RX MEDLINE=97236426; PubMed=9116031;

RA Beck M., Mueller D., Bigl V.;
 RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
 alternative splicing";
 RL Biochim Biophys Acta 1351:17-21(1997).
 DR EMBL: X87631; CA66230.1; -.
 DR HSSP: P05067; 1BA4.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PRO0203; AMYLOIDA.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 SQ SEQUENCE 693 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 100.0%; Score 47; DB 11; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10
 |||
 DB 589 EEISEVKMDA 598

RESULT 10
 Q9TUI0 PRELIMINARY; PRT; 770 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13; Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE AMYLOID PRECURSOR PROTEIN.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kimura A., Takahashi T.;
 RT "Amyloid Precursor Protein 770.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB032550; BAA84580.1; -.
 DR HSSP: P05067; 1AAP.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PRO0203; AMYLOIDA.
 DR PRINTS: PRO0759; BASICPTASE.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor.
 SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BCC583E CRC64;

Query Match 100.0%; Score 47; DB 6; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.59;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10
 |||
 DB 664 EEISEVKMDA 673

RESULT 11

ID 093296 PRELIMINARY; PRT; 534 AA.

AC 093296;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE AMYLOID PROTEIN (FRAGMENT).

OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:98337885; PubMed:9671674;
 RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
 RA Milligan C.E.;
 RT "Increased production of amyloid precursor protein provides a
 substrate for caspase-3 in dying motoneurons";
 RL J. Neurosci. 18:5869-5880(1998).
 DR EMBL: AF042098; AAC25052.1; -.
 DR HSSP: P05067; 1BA4.
 DR InterPro: IPR001868; A4_APP.
 DR PRINTS: PRO0203; AMYLOIDA.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 FT NON_TER 1
 SQ SEQUENCE 534 AA; 60597 MW; FB53EC2E66D4C92 CRC64;

Query Match 97.9%; Score 46; DB 13; Length 534;
 Best Local Similarity 90.0%; Pred. No. 0.64;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10
 |||
 DB 428 EEISEVKMDA 437

RESULT 12
 Q9PVL1 PRELIMINARY; PRT; 569 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE AMYLOID PROTEIN (FRAGMENT).
 GN APP.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Coulson E.J., Palla K., Beyreuther K., Masters C.L.;
 RT "What the evolution of the amyloid protein precursor supergene family
 tells us about its function";
 RL Neurochem. Int. 0:0-0(2000).
 DR EMBL: AF030341; AAF12698.1; -.
 DR HSSP: P05067; 1BA4.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PRO0203; AMYLOIDA.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 FT NON_TER 1
 SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match 97.9%; Score 46; DB 13; Length 569;
 Best Local Similarity 90.0%; Pred. No. 0.68;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10
 |||
 DB 464 EEISEVKMDA 473

RESULT 13
Q9DGJ8 PRELIMINARY; PRT; 695 AA.
AC Q9DGJ8; 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID-9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolose A., Sorribas V.:
RT "Cloning of full-length chicken beta-amyloid precursor protein
isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289218; AAC00593.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F20LED02AEC86D95 CRC64;

Query Match 97.9%; Score 46; DB 13; Length 695;
Best Local Similarity 90.0%; Pred. No. 0.84;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEISEVKMDA 10
Db 589 EEVSEVKMDA 598
|||||

RESULT 14
Q9DGJ7 PRELIMINARY; PRT; 751 AA.
AC Q9DGJ7; 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID-9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolose A., Sorribas V.:
RT "Cloning of full-length chicken beta-amyloid precursor protein
isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289219; AAC00594.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 97.9%; Score 46; DB 13; Length 751;
Best Local Similarity 90.0%; Pred. No. 0.91;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EEISEVKMDA 10
Db 645 EEVSEVKMDA 654
|||||

RESULT 15
Q98SG0 PRELIMINARY; PRT; 693 AA.
AC Q98SG0; 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE BETA-AMYLOID PRECURSOR PROTEIN A.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID-8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
University of Nijmegen, Nijmegen, Netherlands.
DR EMBL; AJ298150; CAC37193.1; -.
DR HSSP; P05067; 1HZ3.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 693 AA; 78568 MW; CAFIDF655C1AB653 CRC64;

Query Match 93.6%; Score 44; DB 13; Length 693;
Best Local Similarity 90.0%; Pred. No. 2.1;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEISEVKMDA 10
Db 587 EEISEVKMDS 596
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Search completed: October 29, 2002, 10:29:37
Job time : 19.1429 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:56 : Search time 9 seconds
(without alignments)
27.140 Million cell updates/sec

Title: US-09-580-018-1
Perfect score: 47
Sequence: 1 EISEVVKMDA 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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6: /cgn2.6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	27	1	US-08-141-324-11
2	47	100.0	27	1	US-08-541-902-11
3	47	100.0	45	1	US-08-462-859A-5
4	47	100.0	45	1	US-08-123-659A-5
5	47	100.0	45	1	US-08-464-247A-5
6	47	100.0	45	1	US-08-464-248A-5
7	47	100.0	58	1	US-08-371-930-25
8	47	100.0	58	5	PCT-US94-01712-25
9	47	100.0	63	1	US-08-462-859A-3
10	47	100.0	63	1	US-08-462-859A-4
11	47	100.0	63	1	US-08-123-659A-3
12	47	100.0	63	1	US-08-123-659A-4
13	47	100.0	63	1	US-08-464-247A-3
14	47	100.0	63	1	US-08-464-247A-4
15	47	100.0	63	1	US-08-464-248A-3
16	47	100.0	63	1	US-08-464-248A-4
17	47	100.0	152	6	5187153-4
18	47	100.0	152	6	5187153
19	47	100.0	162	6	5220013-4
20	47	100.0	162	6	5220013
21	47	100.0	264	1	US-07-990-893-5
22	47	100.0	487	1	US-08-462-859A-9
23	47	100.0	487	1	US-08-123-659A-9
24	47	100.0	487	1	US-08-464-247A-9
25	47	100.0	487	1	US-08-464-248A-9
26	47	100.0	492	1	US-08-462-859A-7
27	47	100.0	492	1	US-08-123-659A-7

28	47	100.0	492	1	US-08-464-248A-7	Sequence 7, Appl1
29	47	100.0	656	1	US-08-371-930-23	Sequence 23, Appl1
30	47	100.0	656	5	PCT-US94-01712-23	Sequence 23, Appl1
31	47	100.0	676	1	US-08-371-930-24	Sequence 24, Appl1
32	47	100.0	676	5	PCT-US94-01712-24	Sequence 24, Appl1
33	47	100.0	694	1	US-08-339-152A-18	Sequence 18, Appl1
34	47	100.0	694	2	US-08-007-999B-5	Sequence 5, Appl1
35	47	100.0	694	2	US-08-689-276A-5	Sequence 5, Appl1
36	47	100.0	695	1	US-08-371-930-27	Sequence 27, Appl1
37	47	100.0	695	1	US-08-123-702-2	Sequence 2, Appl1
38	47	100.0	695	1	US-08-339-152A-30	Sequence 30, Appl1
39	47	100.0	695	2	US-08-104-165-1	Sequence 1, Appl1
40	47	100.0	695	3	US-08-464-250-1	Sequence 1, Appl1
41	47	100.0	695	4	US-08-464-250-1	Sequence 1, Appl1
42	47	100.0	695	4	US-09-458-481B-4	Sequence 4, Appl1
43	47	100.0	695	4	US-09-458-481B-6	Sequence 6, Appl1
44	47	100.0	695	4	US-09-458-481B-6	Sequence 6, Appl1
45	47	100.0	695	4	US-09-458-481B-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-08-141-324-11
Sequence 11, Application US/08141324
Patent No. 5475097
GENERAL INFORMATION:
APPLICANT: Travisa, James
APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Nadine
APPLICANT: Pike, Robert N.
TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
TITLE OF INVENTION: Protease
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,324
FILING DATE: 21-Oct-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 44-93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-141-324-11
Query Match 100.0%; Score 47; DB 1; Length 27;
Best local Similarity 100.0%; Pred. No. 0.0047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVVKMDA 10
| | | | | | | | | |
Db 1 EISEVVKMDA 10

RESULT 2

US-08-541-902-11
; Sequence 11, Application US/08541902
; Patent No. 5707620
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,902
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-541-902-11
Query Match 100.0%; Score 47; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVVKMDA 10
| | | | | | | | | |
Db 1 EISEVVKMDA 10

RESULT 3

US-08-462-859A-5
; Sequence 5, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3305
; TELEFAX: (201)831-3246
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-462-859A-5
Query Match 100.0%; Score 47; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVVKMDA 10
| | | | | | | | | |
Db 2 EISEVVKMDA 11

RESULT 4

US-08-123-659A-5
; Sequence 5, Application US/08123659A
; Patent No. 5656477
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Rosenblum
; STREET: 163 Delaware Avenue, Suite 212
; CITY: Delmar
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 12054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,659A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenblum, Anne M.

REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-5

Query Match 100.0%; Score 47; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 E1E1SEVKMDA 10
Db 2 E1E1SEVKMDA 11

RESULT 5
US-08-464-247A-5
Sequence 5, Application US/08464247A
Patent No. 5693478

GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-4117
TELEFAX: 201-683-2158
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-5

Query Match 100.0%; Score 47; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 E1E1SEVKMDA 10
Db 2 E1E1SEVKMDA 11

RESULT 6
US-08-464-248A-5
Sequence 5, Application US/08464248A
Patent No. 5703209

GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5703209e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-5

Query Match 100.0%; Score 47; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 E1E1SEVKMDA 10
Db 2 E1E1SEVKMDA 11

RESULT 7
US-08-371-930-25
Sequence 25, Application US/08371930
Patent No. 5578451
GENERAL INFORMATION:
APPLICANT: Nishimoto, Ikuro
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)

;; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,930
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-371-930-25

Query Match 100.0%; Score 47; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEISEVKMDA 10
Db 39 EEISEVKMDA 48

;; RESULT 8
; PCT-US94-01712-25
; Sequence 25, Application PC/TUS9401712
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuro
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; OPERATING SYSTEM: IBM PS/2 Model 502 or 55SX
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01712
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PCT-US94-01712-25

Query Match 100.0%; Score 47; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEISEVKMDA 10
Db 39 EEISEVKMDA 48

;; RESULT 9
; US-08-462-859A-3
; Sequence 3, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5652092a1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-462-859A-3

Query Match 100.0%; Score 47; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEISEVKMDA 10
Db 2 EEISEVKMDA 11

;; RESULT 10
; US-08-462-859A-4
; Sequence 4, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5652092a1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; NUMBER OF SEQUENCES: 19

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: American Cyanamid Company
;; STREET: One Cyanamid Plaza
;; CITY: Wayne
;; STATE: New Jersey
;; COUNTRY: United States
;; ZIP: 07470-8426
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patent Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/462,859A
;; FILING DATE: 05-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Barnhard, Elizabeth M.
;; REGISTRATION NUMBER: 31,088
;; REFERENCE/DOCKET NUMBER: 31,844-04
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (201)831-3246
;; TELEFAX: (201)831-3305
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 63 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-462-859A-4

Query Match 100.0%; Score 47; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVVKMDA 10
|||
Db 2 EISEVVKMDA 11

RESULT 11
US-08-123-659A-3
; Sequence 3, Application US/08123659A
; Patent No. 5656477
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; TITLE OF INVENTION: No. 5656477e1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Rosenblum
; STREET: 163 Delaware Avenue, Suite 212
; CITY: Delmar
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 12054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,659A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenblum, Anne M.
; REGISTRATION NUMBER: 30,419
; REFERENCE/DOCKET NUMBER: 31,844-01
; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (518)475-0611
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 63 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-123-659A-3

Query Match 100.0%; Score 47; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVVKMDA 10
|||
Db 2 EISEVVKMDA 11

RESULT 12
US-08-123-659A-4
; Sequence 4, Application US/08123659A
; Patent No. 5656477
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; TITLE OF INVENTION: No. 5656477e1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Rosenblum
; STREET: 163 Delaware Avenue, Suite 212
; CITY: Delmar
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 12054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,659A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenblum, Anne M.
; REGISTRATION NUMBER: 30,419
; REFERENCE/DOCKET NUMBER: 31,844-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (518)475-0611
; TELEFAX: (518)475-0619
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-123-659A-4

Query Match 100.0%; Score 47; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVVKMDA 10
|||
Db 2 EISEVVKMDA 11

RESULT 13
US-08-464-247A-3
; Sequence 3, Application US/08464247A

```
; Patent No. 5693478
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,247A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-247A-3

Query Match          100.0%; Score 47; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10
Db 2 EEISEVKMDA 11

RESULT 14
US-08-464-247A-4
; Sequence 4, Application US/08464247A
; Patent No. 5693478
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

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; APPLICATION NUMBER: US/08/464,247A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-247A-4

Query Match          100.0%; Score 47; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEISEVKMDA 10
Db 2 EEISEVKMDA 11

RESULT 15
US-08-464-248A-3
; Sequence 3, Application US/08464248A
; Patent No. 5703209
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5703209e1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne Jersey
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,248A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-248A-3

Query Match          100.0%; Score 47; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.012;
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Matches	10;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	EEISEVKMDA	10						
DB	2	EEISEVKMDA	11						

Search completed: October 29, 2002, 10:32:06
Job time : 10 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:21 ; Search time 23.1429 Seconds

(without alignments)
47.995 Million cell updates/sec

Title: us-09-580-018-2
Perfect score: 47
Sequence: 1 EISEVKMDAF-10

Scoring table: BLAST62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A Geneseq_032802:*

- 1: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
- 2: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
- 3: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
- 4: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
- 5: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
- 6: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
- 7: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
- 8: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
- 9: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
- 10: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
- 11: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
- 12: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
- 13: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
- 14: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
- 15: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
- 16: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
- 17: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
- 18: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
- 19: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
- 20: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
- 21: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	10	22	AA046206 Human APP derived
2	47	100.0	13	19	AA070869 Beta-amyloid pepit
3	47	100.0	16	21	AA06315 Human beta-amyloid
4	47	100.0	18	22	AA060608 Beta-amyloid precu
5	47	100.0	20	21	AA069713 Beta-APP alpha-sec
6	47	100.0	33	20	AA098002 Amyloid precursor
7	47	100.0	39	21	AA069717 Beta-APP alpha-sec
8	47	100.0	45	18	AA026512 Amyloid precursor
9	47	100.0	45	18	AA026392 Amyloid precursor
10	47	100.0	45	19	AA044748 APP-REP 751 [BAP d
11	47	100.0	45	19	AA042977 Deletion beta-amy1

12	47	100.0	53	16	AA064168 Variant beta amylo
13	47	100.0	57	21	AA010910 Human amyloid prec
14	47	100.0	58	15	AA058937 Amyloid precursor
15	47	100.0	63	18	AA026511 Amyloid precursor
16	47	100.0	63	18	AA026391 Amyloid precursor
17	47	100.0	63	19	AA044747 APP-REP 751 BAP pe
18	47	100.0	63	19	AA044746 APP-REP 751 [BAP E
19	47	100.0	63	19	AA042975 Beta-amyloid pepit
20	47	100.0	63	19	AA042976 Beta-amyloid pepit
21	47	100.0	67	19	AA071377 Peptide derived fr
22	47	100.0	93	22	AB019083 Novel human diagno
23	47	100.0	112	17	AA093556 Familial Alzheimer
24	47	100.0	115	20	AA097999 London-FAD APP pol
25	47	100.0	162	9	AA083151 Deduced sequence 1
26	47	100.0	162	12	AA037863 Beta-amyloid-relat
27	47	100.0	162	14	AA037863 Deduced from clone
28	47	100.0	249	15	AA065798 Beta-amyloid precu
29	47	100.0	264	10	AA090497 Protein sequence 1
30	47	100.0	264	10	AA090609 Sequence of amy 37
31	47	100.0	487	18	AA026510 Amyloid precursor
32	47	100.0	487	18	AA026394 Amyloid precursor
33	47	100.0	487	19	AA044745 APP-REP 751 protei
34	47	100.0	487	19	AA042979 Amyloid precursor
35	47	100.0	492	14	AA045229 APP-REP 751 amyloi
36	47	100.0	492	18	AA026509 Amyloid precursor
37	47	100.0	492	18	AA026393 Amyloid precursor
38	47	100.0	492	19	AA044744 APP-REP 751 protei
39	47	100.0	492	19	AA042978 Amyloid precursor
40	47	100.0	537	14	AA040114 APP-HCV-E2 fusion
41	47	100.0	596	15	AA065797 Beta-amyloid precu
42	47	100.0	627	21	AA010955 SEAP/human amyloid
43	47	100.0	651	15	AA065796 Beta-amyloid precu
44	47	100.0	656	15	AA058935 Amyloid precursor
45	47	100.0	670	15	AA065795 APP751 beta-amyloi

ALIGNMENTS

RESULT 1

AA046206 standard; peptide; 10 AA.

04-APR-2001 (first entry)

Human APP derived immunogenic peptide #2.

XX Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;
XX Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
XX amyloid precursor protein; Alzheimer's disease.

XX Homo sapiens.

XX WO200072880-A2.

XX PD 07-DEC-2000.

XX PF 26-MAY-2000; 2000WO-US14810.

XX PR 28-MAY-1999; 99US-0322289.

XX PA (NEUR-) NEURALAB LTD.

XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;

XX WPI; 2001-032104/04.

XX DR Preventing or treating a disease associated with amyloid deposits,

XX PT especially Alzheimer's disease, comprises administering amyloid

XX specific antibody

PS Disclosure: Figure 19; 143pp; English.

CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have neurotropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease.

SQ Sequence 10 AA:

Query Match 100.0%; Score 47; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
|
Db 1 EISEVKMDAE 10

RESULT 2

ID AAM70869 standard; peptide; 13 AA.

AC AAM70869;

DT 04-FEB-1999 (first entry)

DE Beta-amyloid peptide to create a monoclonal antibody.

KW Beta-amyloid precursor protein; beta-APP; beta-amyloid peptide;
KW antibody; amyloid deposit; Alzheimer's disease.

OS Synthetic.

OS Homo sapiens.

PN W03844955-A1.

PD 15-OCT-1998.

PF 09-APR-1998; 98WO-US06900.

PR 09-APR-1997; 97US-0041850.

PA (MCIN/) MCINNIS P. A.
PA (MIND-) MINDSER LTD.

F1 Chain DG;

DR WPI; 1998-594476/50.

PT Preventing or inhibiting progression of Alzheimer's Disease -
PT comprises use of recombinant DNA encoding an antibody specific for
PT the N- or C-terminus of an amyloid-beta peptide

XX Example 1; Page 47; 58pp; English.

XX The present sequence represents a peptide derived from beta-amyloid
CC precursor protein (beta-APP). The peptide is a beta-amyloid
CC peptide and is used to produce a monoclonal antibody. The specification
CC describes a method for prevention or inhibition of progression of
CC Alzheimer's disease. The method comprises administering a composition
CC comprising a recombinant DNA molecule containing a gene encoding a
CC recombinant antibody end-specific for the N-terminus or the C-terminus
CC of an amyloid-beta peptide, operably linked to a promoter which is
CC expressed in the central nervous system. The recombinant antibody

CC molecules prevent the accumulation of beta-amyloid peptides in the
CC extracellular space, interstitial fluid and cerebrospinal fluid and the
CC aggregation of such peptides into amyloid deposits in the brain. They
CC also inhibit the progression of Alzheimer's disease by inhibiting the
CC interaction of beta-amyloid peptides mediating Alzheimer's disease
CC induced neurotoxicity and inhibiting the Alzheimer's disease induced
CC complement activation and cytokine release involved in the inflammatory
CC process.

SQ Sequence 13 AA:

Query Match 100.0%; Score 47; DB 19; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
|
Db 1 EISEVKMDAE 10

RESULT 3
AAB06315
ID AAB06315 standard; peptide; 16 AA.

AC AAB06315;

DT 03-OCT-2000 (first entry)

DE Human beta-amyloid precursor protein beta-secretase cleavage site.

KW Human; beta-amyloid precursor protein; beta-APP; beta-secretase;
KW subtilisin-kexin isoenzyme 1; SKI-1;

KW pro-brain-derived neurotrophic factor; proBDNF; anti11pemic;
KW cytosolic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia;

KW liver steatosis; Ras-dependent cancer; restenosis;
KW amyloid protein formation.

OS Homo sapiens.

OS Key Location/Qualifiers

FT Cleavage-site 8..9

PN W0200026348-A2.

PD 11-MAY-2000.

PF 04-NOV-1999; 99WO-CA01058.

PR 04-NOV-1998; 98CA-2249648.

PA (RECL-) INST RECH CLINIQUES MONTREAL.

PI Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

DR WPI; 2000-365601/31.

PT Novel soluble proteic fragment of subtilisin-kexin isoenzyme for
PT producing a polypeptide useful for treating hypercholesterolemia, liver
PT steatosis and amyloidosis, comprises a specific amino acid sequence -
XX Example 4; Page 51; 119pp; English.

XX The present sequence is the beta-secretase site of human beta-amyloid
CC precursor protein (beta-APP). The sequence may be cleaved
CC by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1
CC (SKI-1), a type-1 membrane-bound protease. Peptides which bind to and
CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for
CC screening inhibitors of SKI-1 activity, or for screening enhancers of
CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1
CC catalytic site may be used as inhibitors of SKI-1 activity. They may be
CC used to treat diseases involving overexpression of SKI-1 or SKI-1
CC substrate. Such diseases include hypercholesterolemia, high levels of
CC fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,

CC Ras-dependent cancer, restenosis and amyloid protein formation.

XX Sequence 16 AA;

Query Match 100.0%; Score 47; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.0042;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10

|||||

Db 2 EISEVKMDAE 11

RESULT 4

AAE00608 ID AAE00608 standard; peptide: 18 AA.

AC AAE00608;

DT 02-JUL-2001 (first entry)

DE Beta-amyloid precursor protein beta-secretase cleavage site.

XX Beta-amyloid precursor protein; beta-APP; caspase; beta-secretase;

KM cysteine protease; apoptosis; caspase expression cassette; metastasis;

KW tumour; cathepsin B; urokinase; proliferation; gene therapy;

KV Interdomain linker; cleavage site; Alzheimer's disease.

XX OS Unidentified.

XX MO200129232-A2.

XX PD 26-APR-2001.

XX PF 19-OCT-2000; 2000MO-US28941.

XX PR 20-OCT-1999; 9905-0160559.

XX PR 14-AUG-2000; 2000US-0225564.

XX PA (SCIO-) SCIOS INC.

XX PI Cordell B, Li Y;

XX DR WPI; 2001-290920/30.

XX PT Novel fusion polypeptide comprising first and second caspase subunit

XX PS separated by cleavage site not associated in nature with caspase

XX PT subunit, useful for cloning gene encoding enzymes involved in

XX PT proteolytic cleavage

XX PS Example 2; Page 26; 116pp; English.

XX CC The present sequence is a beta-secretase cleavage site of beta-amyloid

CC precursor protein (beta-APP). This sequence is used to construct

CC an artificially engineered chimeric cassette comprising human caspase-3

CC with interdomain linker replaced by swedish mutant beta-secretase

CC cleavage site. This modified caspase-3 plays a pivotal role in

CC Alzheimer's disease. Caspases are a family of cysteine proteases, that

CC participate in the initiation and execution of apoptosis.

CC The present invention relates to a method for functional cloning of genes

CC encoding proteins or enzymes involved in proteolytic cleavage. The

CC invention is based on the use of caspase expression cassettes comprising

CC the coding sequence of a proteolytic cleavage site flanked by sequences

CC encoding two caspase subunits. A fusion polypeptide comprising a first

CC and a second caspase subunit, separated by a cleavage site not associated

CC in nature, is useful for cloning gene encoding enzymes involved in

CC proteolytic cleavage. An expression cassette containing fusion

CC polypeptide is used to identify a mutant cell line deficient in an

CC enzyme of interest and is also useful for diagnosis and suppression of

CC proliferation or metastases of a tumour cell characterized by

CC overexpression of a polypeptide (e.g. Cathepsin B or urokinase,

CC selectively expressed in the tumour cells). DNA encoding fusion

CC polypeptide is used in gene therapy.

XX Sequence 18 AA;

Query Match 100.0%; Score 47; DB 22; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.0048;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10

|||||

Db 4 EISEVKMDAE 13

RESULT 5

AAV69713 ID AAV69713 standard; peptide: 20 AA.

AC AAV69713;

DT 11-APR-2000 (first entry)

DE Beta-APP alpha-secretase substrate [KW]-APP(-10,+10).

XX Neurotrophic; neuroprotective; beta-amyloid precursor protein; metabolism;

KM cleavage site; beta-secretase; neurodegenerative disease;

KW Alzheimer's disease.

XX OS Homo sapiens.

XX MO9964587-A1.

XX PD 16-DEC-1999.

XX PF 04-JUN-1999; 99MO-FR01326.

XX PR 05-JUN-1998; 98PR-0007068.

XX PR 31-MAR-1999; 99US-0122599.

XX PA (RHON) RHONE-FOULENC RORER SA.

XX PA (UYPA-) UNIV CURIE PARIS VI P & M.

XX PI Rholam M, Munoz-Gimenez N, Moutouakil M, Cohen P, Bertrand P;

XX DR WPI; 2000-097537/08.

XX PT Polypeptide with beta-secretase activity, specific for wild-type

XX PT amyloid precursor protein, useful in treating Alzheimer's disease

XX PS Example 3; Page 24; 44pp; French.

XX CC Peptides AAV69702-Y69718 represent synthetic peptide substrates for a

CC novel polypeptide with beta-secretase activity that can cleave

CC specifically the natural beta-amyloid precursor protein (bAPP). Normal

CC cleavage of the protein occurs between amino acids Met596-Asp597 and

CC Val638-Ile637 (positions 4-5 and 44-45 of AAV69701). The novel

CC polypeptide is used to identify agents that interact specifically with

CC it. These agents regulate metabolism of APP, particularly they slow down

CC or reduce production of beta-amyloid, so can be used to treat

CC neurodegenerative diseases, particularly Alzheimer's disease.

XX SQ Sequence 20 AA;

Query Match 100.0%; Score 47; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.0054;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10

|||||

Db 4 EISEVKMDAE 13

RESULT 6

AAW98002 ID AAW98002 standard; protein: 33 AA.

```

XX AC AAW98002;
XX XX 21-JUN-1999 (first entry)
XX XX
XX DE Amyloid precursor protein (aa656-678) with Swedish mutation.
XX XX
XX KW Amyloid precursor protein; APP; human; gene targeting;
XX KW homologous recombination; transgenic mouse; transgenic animal;
XX KM animal model; Alzheimer's disease.
XX XX
XX OS Mus musculus.
XX XX
XX PN M09909150-A1.
XX XX
XX PD 25-FEB-1999.
XX XX
XX PF 18-AUG-1997; 97WO-US14507.
XX XX
XX PR 18-AUG-1997; 97WO-US14507.
XX XX
XX PA (FARB ) BAYER CORP.
XX XX
XX PI Wirak DO;
XX XX
XX DR WPI: 1999-181029/15.
XX XX
XX PT Modification of target nucleic acids - by homologous recombination,
XX PT used particularly for introducing a humanised amyloid precursor
XX PT protein gene into rodents for producing models of Alzheimer's
XX PT disease
XX XX
XX PS Disclosure; Page 145; 209pp; English.
XX XX
XX CC This polypeptide comprises residues 656-678 of a murine amyloid
XX CC precursor protein (APP). The invention provides a novel gene
XX CC targeting strategy that facilitates the introduction of one or
XX CC more specific mutations into any gene in a single double reciprocal
XX CC homologous recombination step. The method has been used
XX CC particularly for introducing a humanised APP gene into rodents for
XX CC producing animal models of Alzheimer's disease (AD). 4 independent
XX CC lines of transgenic mice (lines ES5007, ES5103, ES5401 and ES5403)
XX CC have been created using the gene targeting technique applied to
XX CC embryonic stem cells. In each line, the mouse APP gene was modified
XX CC to encode a mouse/human hybrid (m/hAPP) where amino acid residues
XX CC 666-770 of APP770 were encoded by human cDNA sequences instead of
XX CC mouse genomic exons (exons 16-18). Within these residues, only 3
XX CC amino acid differences exist between the mouse and human proteins,
XX CC i.e. Gly-676 to Arg, Phe-681 to Thr and Arg-684 to His. The
XX CC exon-cDNA fusion gene therefore encodes an APP containing a
XX CC humanised beta-amyloid domain. Swedish- and/or London-FAD APP
XX CC mutations have also been introduced (see also AAW97997-W98001).
XX XX
XX SQ Sequence 33 AA;

Query Match 100.0%; Score 47; DB 20; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EISEVKMDAE 10
DB 10 EISEVKMDAE 19

RESULT 7
AAV69717
ID AAV69717 standard; peptide: 39 AA.
XX AC AAV69717;
XX XX
XX DF 11-APR-2000 (first entry)
XX XX
XX DE Beta-APP alpha-secretase substrate [KM]-APP(-20,+20).

```

```

XX XX
XX KW Neotropic; neuroprotective; beta-amyloid precursor protein; metabolism;
XX KW cleavage site; beta-secretase; neurodegenerative disease;
XX KM Alzheimer's disease.
XX XX
XX OS Homo sapiens.
XX XX
XX PN M09964587-A1.
XX XX
XX PD 16-DEC-1999.
XX XX
XX PF 04-JUN-1999; 99WO-FR01326.
XX XX
XX PR 05-JUN-1998; 98FR-0007068.
XX PR 31-MAR-1999; 99US-0122599.
XX XX
XX PA (RHON ) RHONE-POULENC RORER SA.
XX PA (UYPA-) UNIV CURIE PARIS VI P 6 M.
XX XX
XX PI Rhoulam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
XX XX
XX DR WPI: 2000-097537/08.
XX XX
XX PT Polypeptide with beta-secretase activity, specific for wild-type
XX PT amyloid precursor protein, useful in treating Alzheimer's disease -
XX XX
XX PS Example 3; Page 24; 44pp; French.
XX XX
XX CC Peptides AAV69702-Y69718 represent synthetic peptide substrates for a
XX CC novel polypeptide with beta-secretase activity that can cleave
XX CC specifically the natural beta-amyloid precursor protein (bAPP). Normal
XX CC cleavage of the protein occurs between amino acids Met596-Asp597 and
XX CC Val636-Ile637 (positions 4-5 and 44-45 of AAV69701). The novel
XX CC polypeptide is used to identify agents that interact specifically with
XX CC it. These agents regulate metabolism of APP, particularly they slow down
XX CC or reduce production of beta-amyloid, so can be used to treat
XX CC neurodegenerative diseases, particularly Alzheimer's disease.
XX XX
XX SQ Sequence 39 AA;

Query Match 100.0%; Score 47; DB 21; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EISEVKMDAE 10
DB 13 EISEVKMDAE 22

RESULT 8
AAW26512
ID AAW26512 standard; peptide: 45 AA.
XX AC AAW26512;
XX XX
XX DF 06-JAN-1998 (first entry)
XX XX
XX DE Amyloid precursor protein fragment APP-RPP 751 (BAP dell1-28).
XX XX
XX KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;
XX KW substrate; mutelin; secretase; Alzheimer's disease; human.
XX XX
XX OS Chimeric Homo sapiens.
XX OS Chimeric synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FH Cleavage-site 7..8
XX FT /note= "secretase cleavage site"
XX FT Peptide 10..33
XX FT /label= BAP(dell1-28)
XX FT /note= "truncated beta-amyloid protein"
XX FT 20..42
XX FT Domain
XX FT /label= Transmembrane

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XX  XX  US5656477-A.
PN  XX
PD  12-AUG-1997.
PF  01-MAY-1992; 92US-0877675.
PR  20-SEP-1993; 93US-0123659.
PR  01-MAY-1992; 92US-0877675.
XX  XX  (AMCY ) AMERICAN CYANAMID CO.
PA  XX
PI  XX  Jacobsen JS, Vitek MP;
DR  WPI; 1997-414594/38.
PT  Nucleic acid encoding amyloid precursor muten(s) - comprising
PT  reporter gene and coding sequence, for identifying compounds which
PT  modify the activity of proteolytic enzymes which cleave APP
XX  XX
PS  Disclosure; Fig 5A; 84pp; English.
XX  XX  This peptide sequence shows the region of amyloid precursor protein
CC  (APP) that includes a truncated beta-amyloid protein (BAP) lacking
CC  the native secretase cleavage/recognition site. In an attempt to
CC  engineer an APP non-cleavable substrate for secretase, an
CC  APP-reporter (APP-REP) protein that carries the BAP deletion has
CC  been expressed in recombinant host cells. Deletion of these 18
CC  amino acids, however, still resulted in the secretion of an
CC  N-terminal APP-reporter fragment into the cytoplasm. Non-
CC  cleavable APP substrates can be used to detect other putative
CC  abnormal APP processing events. They can also be used to
CC  investigate cellular post-translational modifications to APP in
CC  order to determine the potential influence on normal secretase and
CC  abnormal BAP 'clipping' activities.
XX  XX
SQ  Sequence 45 AA;
Query Match 100.0%; Score 47; DB 18; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EISEVKMDAE 10
    |||||||
DB 3 EISEVKMDAE 12

RESULT 9
ID AAW26392 standard; Peptide; 45 AA.
XX
AC AAW26392;
XX
DT 15-DEC-1997 (first entry)
XX
DE Amyloid precursor protein fragment APP-REP 751 (BAP del11-28).
XX
KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KW substrate; muten; secretase; Alzheimer's disease; human.
XX
OS Chimeric Homo sapiens;
OS Chimeric synthetic.
XX
FH Key Location/Qualifiers
FT Cleavage-site 7..8 /note= "secretase cleavage site"
FT Peptide 10..33 /label= BAP(del11-28)
FT /note= "truncated beta-amyloid protein"
FT Domain 20..42 /label= Transmembrane
FT
XX
PN US5652092-A.

```

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XX  XX  29-JUL-1997.
PD  XX
PF  01-MAY-1992; 92US-0877675.
PR  20-SEP-1993; 93US-0123659.
PR  01-MAY-1992; 92US-0877675.
PR  05-JUN-1995; 95US-0462859.
XX  XX  (AMCY ) AMERICAN CYANAMID CO.
PA  XX
PI  XX  Jacobsen JS, Vitek MP;
DR  WPI; 1997-392937/36.
PT  Screening for compounds which reduce beta-amyloid protein formation
PT  - using cells which express a construct encoding a marker and an
PT  amyloid precursor muten derived from APP isoforms
XX  XX
PS  Disclosure; Fig 5A; 84pp; English.
XX  XX  This peptide sequence shows the region of amyloid precursor protein
CC  (APP) that includes a truncated beta-amyloid protein (BAP) lacking
CC  the native secretase cleavage/recognition site. In an attempt to
CC  engineer an APP non-cleavable substrate for secretase, an
CC  APP-reporter (APP-RBP) protein that carries the BAP deletion has
CC  been expressed in recombinant host cells. Deletion of these 18
CC  amino acids, however, still resulted in the secretion of an
CC  N-terminal APP-reporter fragment into the cytoplasm. Non-
CC  cleavable APP substrates can be used to detect other putative
CC  abnormal APP processing events. They can also be used to
CC  investigate cellular post-translational modifications to APP in
CC  order to determine the potential influence on normal secretase and
CC  abnormal BAP 'clipping' activities.
XX  XX
SQ  Sequence 45 AA;
Query Match 100.0%; Score 47; DB 18; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EISEVKMDAE 10
    |||||||
DB 3 EISEVKMDAE 12

RESULT 10
ID AAW4748 standard; Protein; 45 AA.
XX
AC AAW4748;
XX
DT 01-JUN-1998 (first entry)
XX
DE APP-RBP 751 [BAP delta(11-28)] peptide.
XX
KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
KW Alzheimer's disease; cleavage.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Cleavage-site 7..8 /note= "putative secretase cleavage site"
FT MISC-difference 19..20 /note= "residues 11-28 of the wild type BAP sequence
FT /note= "are deleted from between these positions"
FT
XX
PN US5693478-A.
XX
PD 02-DEC-1997.

```

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XX 05-JUN-1995: 950S-0464247.
PF 20-SEP-1993: 930S-0123659.
XX 01-MAY-1992: 920S-0877675.
PR 05-JUN-1995: 950S-0464247.
XX
PA (AMCY ) AMERICAN CYANAMID CO.
XX
PI Jacobsen JS, Vitek MP;
XX
DR WPI: 1998-031744/03.
XX
PT Amyloid precursor muten reporter molecule assay containing antibody
PT recognised marker - used to study pathways associated with
PT Alzheimer's disease
XX
PS Disclosure: Fig 5A; 84pp; English.
XX
CC This sequence represent the beta-amyloid protein sequence from the
CC construct APP-REP751 (BAP delta(11-28)). The mutant sequence contains
CC a deletion of the wild type BAP residues 11-28. This causes a
CC shortening of the BAP sequence. This may affect cleavage of the BAP by
CC the "secretase" dependent on whether the "secretase" recognises the
CC cleavage site by a positional effect or by sequence. The mutant sequence
CC can be used in a method to study secretase and beta-amyloid protein
CC (BAP)-generating pathways associated with Alzheimer's disease by
CC studying proteolytic cleavage of the reporter polypeptides (e.g.
CC AAM44744 and AAM44745).
XX
SQ Sequence 45 AA:
Query Match 100.0%; Score 47; DB 19; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EISEVKMDAE 10
Db 3 EISEVKMDAE 12

RESULT 11
AAM42977
ID AAM42977 standard; peptide; 45 AA.
XX
AC AAM42977;
XX
DT 01-MAY-1998 (first entry)
XX
DE Deletion beta-amyloid peptide (BAP) derived from APP-REP 751.
XX
KW Beta-amyloid peptide; BAP; extracellular BAP plaque;
KW cerebrovascular deposit; Alzheimers disease; Down's syndrome;
KW amyloid precursor protein; APP; secretase; BAP aggregation;
KW abnormal proteolytic cleavage.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 20..43
FT /note= "putative transmembrane domain"
XX
XX US5703209-A.
XX
XX 30-DEC-1997.
XX
XX 05-JUN-1995: 950S-0464248.
XX
XX 20-SEP-1993: 930S-0123659.
XX 01-MAY-1992: 920S-0877675.
XX
XX (AMCY ) AMERICAN CYANAMID CO.
XX

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PI Jacobsen JS, Vitek MP;
XX
DR WPI: 1998-076482/07.
XX
PT Amyloid precursor protein fusion polypeptides - comprising APP
PT fragment and marker, useful for research and drug screening
XX
PS Disclosure: Fig 5A; 84pp; English.
XX
CC The present sequence represents a beta-amyloid peptide (BAP), with
CC a deletion amino acids 11-28 (numbered according to AAM42976). Abnormal
CC accumulation of extracellular BAP in plaques and cerebrovascular
CC deposits is characteristic in brains of individuals suffering from
CC Alzheimers disease and Down's syndrome. BAP is a poorly soluble,
CC self-aggregating protein which is derived from a larger amyloid precursor
CC protein (APP). APP is expressed as an integral membrane protein, and is
CC cleaved by secretase, between BAP 16lys and 17leu. Cleavage at this site
CC precludes amyloidogenesis and results in the release of the
CC amino-terminal APP fragment. Three major isoforms of APP exist: APP-695,
CC APP-751 and APP-770. These isoforms are derived by alternative splicing.
CC APP-APP 751 is a deletion construct of APP-751, which has a deletion of
CC 276 amino acids to within 15 amino acids of the BAP domain. APP can be
CC used as a substrate for studying abnormal proteolytic cleavage which
CC results in the release of BAP, and also to screen for drugs that will
CC inhibit such cleavage.
XX
SQ Sequence 45 AA:
Query Match 100.0%; Score 47; DB 19; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EISEVKMDAE 10
Db 3 EISEVKMDAE 12

RESULT 12
AAR64168
ID AAR64168 standard; peptide; 53 AA.
XX
AC AAR64168;
XX
DT 02-AUG-1995 (first entry)
XX
DE Variant beta amyloid protein with 10 preceeding amino acids of APP.
XX
KW beta amyloid protein; mutant; variant; detection; amyloid deposition;
KW diagnosis; amyloidosis associated disease; Alzheimer's disease;
KW Down's syndrome; APP; amyloid precursor protein.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..10
FT /note= "the preceeding 10 amino acids of APP"
FT Peptide 11..53
FT /note= "beta amyloid protein variant"
XX
XX W09428412-A.
XX
XX 08-DEC-1994.
XX
XX 27-MAY-1994: 94MO-US05809.
XX
XX 28-MAY-1993: 93US-0069010.
XX
XX (MIRI-) MIRIAM HOSPITAL.
XX PA
XX PA Majocha RE, Marotta CA;
XX PI
XX DR WPI: 1995-023013/03.
XX

```


PT Amyloid binding composition comprising labelled amyloid protein
 PT and carrier - useful for in vivo imaging of amyloid deposits, for
 PT diagnosing Alzheimer's disease and Down's Syndrome.
 XX
 PS Claim 5; Page 43; 58pp; English.
 CC
 CC AAR64168 shows the amino acid sequence of the beta amyloid protein
 CC plus the 10 amino acids preceding the amyloid precursor protein. The
 CC protein binds amyloid and is useful for in vivo imaging of amyloid
 CC deposits and hence diagnosis of an amyloidosis-associated disease, such
 CC as Alzheimer's disease or Down's syndrome. AAR64165 shows the generic
 CC sequence of the amyloid protein for generation of variants.
 CC
 SQ Sequence 53 AA;
 Query Match 100.0%; Score 47; DB 16; Length 53;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EISEVKMDAE 10
 |||||
 DB 4 EISEVKMDAE 13
 RESULT 13
 AABI0910
 ID AABI0910 standard; peptide: 57 AA.
 XX
 AC AABI0910;
 XX
 DT 30-JAN-2001 (first entry)
 XX
 DE Human amyloid precursor APP770 A-beta1-40/42 protein fragment.
 XX
 KM APP; amyloid precursor protein; APP770; human; copper agonist; treatment;
 KM amyloid-beta-peptide; neurotropic; neuroprotective; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN DE1990357-A1.
 XX
 PD 07-SEP-2000.
 XX
 PF 03-MAR-1999; 99DE-1009357.
 XX
 PR 03-MAR-1999; 99DE-1009357.
 XX
 PA (MULT/) MULTHAUP G.
 PA (BEYR/) BEYREUTHER K.
 XX
 PI Beyreuther K, Multaup G, Masters CL;
 XX
 DR WPI: 2000-595035/57.
 XX
 PT Copper agonist binds to the copper binding site of amyloid precursor
 PT protein, useful for treating Alzheimer's disease -
 XX
 PS Example 1; Fig 1; 14pp; German.
 CC
 CC This invention describes a novel copper agonist (I) capable of binding to
 CC the copper binding site of an amyloid precursor protein (APP) and/or
 CC preventing or reducing the release of amyloid-beta-peptides. The
 CC invention also describes (1) a medicament comprising (I) in combination
 CC with a carrier; (2) identifying (I), comprising: (a) contacting potential
 CC (I) with APP; and (b) detecting a reduction of Abeta-proteins; and (3)
 CC identifying (I) comprising: (a) contacting APP or the copper-binding
 CC site-carrying fragment with a solution of, immobilized substance
 CC libraries of, or low molecular weight substances from microorganisms or
 CC plants; (b) performing a competitive assay by adding copper ions to form
 CC complexes with the ligands; (c) identifying the ligands; and (d)
 CC selecting ligands, which bind the APP copper binding site or which reduce
 CC the Abeta peptide release. The products of the invention have neurotropic
 CC and neuroprotective activity. (I) and the resulting medicament are used

CC for preventing or treating Alzheimer's disease.
 XX
 SQ Sequence 57 AA;
 Query Match 100.0%; Score 47; DB 21; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EISEVKMDAE 10
 |||||
 DB 7 EISEVKMDAE 16
 RESULT 14
 AAR58937
 ID AAR58937 standard; peptide: 58 AA.
 XX
 AC AAR58937;
 XX
 DT 15-APR-1995 (first entry)
 XX
 DE Amyloid precursor protein residues 551-608.
 XX
 KM Amyloid precursor protein; beta amyloid; monoclonal antibody;
 KM Anti-Alz 90; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO9416692-A.
 XX
 PD 01-SEP-1994.
 XX
 PF 17-FEB-1994; 94WO-US01712.
 XX
 PR 18-FEB-1993; 93US-0019208.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 XX
 PI Nishimoto I;
 XX
 DR WPI: 1994-294486/36.
 XX
 PT Identifying cpds. useful for treating or preventing Alzheimer's
 PT disease - by determining whether it interferes with the
 PT association of the couplone portion of amyloid precursor protein
 PT to G polypeptide
 XX
 PS Disclosure; Page 40-41; 71pp; English.
 XX
 CC Beta amyloid is synthesised as part of a larger protein referred to
 CC as amyloid precursor protein (APP), which has a number of isoforms
 CC in humans, including APP695 and APP770. APP forms a complex with Go,
 CC a GTP-binding protein (or "G protein") in brain. It is suggested
 CC that abnormal APP-go signalling is involved in the Alzheimer's
 CC disease process. Anti-Alz 90 is a mouse monoclonal antibody
 CC specific for an epitope corresp. to residues 551-608 of APP,
 CC a section of APP that is within the extracellular domain.
 CC
 SQ Sequence 58 AA;
 Query Match 100.0%; Score 47; DB 15; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EISEVKMDAE 10
 |||||
 DB 40 EISEVKMDAE 49
 RESULT 15
 AAW26511
 ID AAW26511 standard; peptide: 63 AA.
 XX

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AC  AAW26511:
XX
DT  06-JAN-1998 (first entry)
XX
DE  Amyloid precursor protein fragment APP-REP 751 (BAP E22Q).
XX
XX  Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KM  substrate; mutelin; secretase; Alzheimer's disease;
XX  hereditary cerebral haemorrhage with amyloidosis; human.
XX
OS  Homo sapiens.
XX
FH  Key Location/Qualifiers
FT  Peptide 10..51
FT  /label= BAP(E22Q)
FT  /note= "beta-amyloid protein E22Q mutant"
FT  Cleavage-site 25..26
FT  /note= "secretase cleavage site"
FT  Domain 38..61
FT  /label= Transmembrane
XX
XX  US5656477-A.
XX  12-AUG-1997.
XX
XX  01-MAY-1992; 92US-0877675.
XX
XX  20-SEP-1993; 93US-0123659.
XX  01-MAY-1992; 92US-0877675.
XX
XX  (AMCY ) AMERICAN CYANAMID CO.
XX
XX  Jacobsen JS, Vittek MP;
XX
XX  WPI: 1997-414594/38.
XX
XX  Nucleic acid encoding amyloid precursor mutelin(s) - comprising
PT  reporter gene and coding sequence, for identifying compounds which
PT  modify the activity of proteolytic enzymes which cleave APP
XX
XX  Disclosure: Fig 5A; 84pp; English.
XX
XX  This peptide sequence shows the region of amyloid precursor protein
CC  (APP) that includes a beta-amyloid protein (BAP) carrying a point
CC  mutation (BAP E22Q) found in patients with hereditary cerebral
CC  haemorrhage with amyloidosis of Dutch origin (HCHWA-D). In an
CC  attempt to engineer an APP non-cleavable substrate for secretase,
CC  an APP-reporter (APP-REP) protein that carries the E22Q mutation
CC  has been expressed in recombinant host cells. This resulted in the
CC  secretion of an N-terminal fragment indistinguishable from that of
CC  APP-REP 751 (see AAW26393-94). Non-cleavable APP substrates can be
CC  used to detect other putative abnormal APP processing events. They
CC  can also be used to investigate cellular post-translational
CC  modifications to APP in order to determine the potential influence
CC  on normal secretase and abnormal BAP 'clipping' activities.
XX
SQ  Sequence 63 AA:

Query Match 100.0%; Score 47; DB 18; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EISEVKMDAE 10
DB 3 EISEVKMDAE 12

```

Search completed: October 29, 2002, 10:26:42
 Job time : 23.1429 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:36 ; Search time 10.4286 Seconds
(without alignments)
92.140 Million cell updates/sec

Title: US-09-580-018-2
Perfect score: 47
Sequence: 1 EISEVKMDAE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR:71:*
2: PIR:2:*
3: PIR:3:*
4: PIR:4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	82	2 PQ0438	Alzheimer's disease
2	47	100.0	695	1 A49795	Alzheimer's disease
3	47	100.0	695	2 A27485	Alzheimer's disease
4	47	100.0	695	2 S00550	Alzheimer's disease
5	47	100.0	770	1 ORH0A4	Alzheimer's disease
6	44	93.6	747	2 JH0773	Alzheimer's disease
7	38	80.9	33	2 S23094	beta-amyloid prote
8	38	80.9	57	2 E60045	Alzheimer's disease
9	38	80.9	57	2 F60045	Alzheimer's disease
10	38	80.9	57	2 G60045	Alzheimer's disease
11	38	80.9	57	2 D60045	Alzheimer's disease
12	38	80.9	57	2 A60045	Alzheimer's disease
13	38	80.9	57	2 B60045	Alzheimer's disease
14	38	80.9	389	2 C64245	MMDH dehydrogenase
15	36	76.6	261	1 C64572	conserved hypotet
16	36	76.6	261	1 F71867	hypothetical prote
17	35	74.5	818	2 AE1598	DNA gyrase-like pr
18	35	74.5	819	2 AG1235	DNA gyrase-like pr
19	34	72.3	590	2 A25680	nuclear histone-bi
20	34	72.3	1378	2 G86837	protein F53H.4 li
21	33	70.2	289	2 T34241	hypothetical prote
22	33	70.2	370	2 T48633	hypothetical prote
23	33	70.2	419	2 D42725	nitrite hydratase
24	33	70.2	626	2 E82273	accessory coloniza
25	33	70.2	743	2 D84854	hypothetical prote
26	33	70.2	793	2 D27133	hypothetical prote
27	33	70.2	800	2 S54427	gyrase-like protei
28	33	70.2	800	2 C89911	topoisomerase IV s
29	32	68.1	146	2 C69136	hypothetical prote

30	32	68.1	389	2 B69096	cortinoid/iron-sul
31	32	68.1	427	2 G84375	adenosylhomocyste
32	32	68.1	427	2 F85436	hypothetical prote
33	32	68.1	470	2 T05258	glycine hydroxymet
34	32	68.1	486	2 AC2424	hypothetical prote
35	32	68.1	632	2 B69310	mRNA 3'-end proces
36	32	68.1	677	2 A695210	sensory transducti
37	32	68.1	679	2 B96599	protein F20N2.12 f
38	32	68.1	690	2 S41009	hypothetical prote
39	32	68.1	705	2 E88564	protein T05G5.9 f1
40	32	68.1	941	2 B96553	hypothetical prote
41	31	66.0	84	2 T27174	hypothetical prote
42	31	66.0	105	2 PH1526	gamma-aminobutyric
43	31	66.0	178	2 C64168	hypothetical prote
44	31	66.0	178	2 C69206	hypothetical prote
45	31	66.0	182	2 AC0449	conserved hypotet

ALIGNMENTS

RESULT 1

PQ0438 Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995

C:Accession: PQ0438; C60045

R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs

A:Reference number: PQ0438; MUID:93075180

A:Accession: PQ0438

A:Molecule type: DNA

A:Residues: 1-82 <DNA>

A:Cross-references: GB:M83558; GB:M83657

R:Ohnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MUID:92017079

A:Accession: C60045

A:Molecule type: mRNA

A:Residues: 12-68 <JOH>

A:Cross-references: EMBL:X56129

C:Species: Macaca fascicularis (cra-b-eating macaque)

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0% Score 47; DB 2; Length 82;

Best Local Similarity 100.0% Pred. No. 0.01;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
Db 10 EISEVKMDAE 19

RESULT 2

A49795 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque

C:Species: Macaca fascicularis (cra-b-eating macaque)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A49795

R:Podlitsny, M.B.; Toljan, D.R.; Selkoe, D.J.

Am. J. Pathol. 138, 1423-1435, 1991

A:Title: Homology of the amyloid beta protein precursor in monkey and human supports

A:Reference number: A49795; MUID:91273117

A:Accession: A49795

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-695 <POD>

A:Cross-references: GB:M58727; NID:9342062; PIDN:AAA36829.1; PID:9342063

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein

C:Keywords: alternative splicing

Query Match 100.0%; Score 47; DB 1; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
 |||||||||
 Db 590 EISEVKMDAE 599

RESULT 3

A27485 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse

N:Alternate names: proteinase nexin II

C:Species: Mus musculus (house mouse)

C>Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999

C:Accession: A27485; S19727; I49485

R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.

Biochem. Biophys. Res. Commun. 149, 665-671, 1987

A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor

A:Reference number: A27485; MUID:88106489

A:Accession: A27485

A:Molecule type: mRNA

A:Residues: 1-695 <YAM>

A:Cross-references: GB:M18373; NID:9191568; PIDN:AAA37139.1; PID:9309085

A:Experimental source: brain

R:de Strooper, B.; van Leuven, F.; van den Berghe, H.

Biochim. Biophys. Acta 1129, 141-143, 1991

A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer

A:Reference number: S19727; MUID:92096458

A:Accession: S19727

A:Molecule type: mRNA

A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>

A:Cross-references: EMBL:X59379

R:Imml, R.; Yamada, T.; Yoshikaki, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.

Gene 112, 189-199, 1992

A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's

A:Reference number: I49485; MUID:92209998

A:Accession: I49485

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-19 <RES>

A:Cross-references: GB:D10603; NID:9220328; PIDN:BA01456.1; PID:9220329

C:Genetics:

A:Map position: 16C3

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase A

C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 100.0%; Score 47; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
 |||||||||
 Db 590 EISEVKMDAE 599

RESULT 4

S00550 Alzheimer's disease amyloid beta protein precursor - rat

N:Alternate names: beta-A4 amyloid protein

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999

C:Accession: S00550; A41245; A39820; S46251

R:Shivers, B.D.; Hildlich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.

EMBO J. 7, 1365-1370, 1988

A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain

A:Reference number: S00550; MUID:88312583

A:Accession: S00550

A:Molecule type: mRNA

A:Residues: 1-695 <SHI>

A:Cross-references: EMBL:X07648; NID:955616; PIDN:CAA30488.1; PID:955617

R:Schubert, D.; Schroeder, R.; Lacordiere, M.; Saitoh, T.; Cole, G.

Science 241, 223-226, 1988

A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan co

A:Reference number: A41245; MUID:88264430

A:Accession: A41245

A:Molecule type: protein

A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>

A>Note: evidence for heparan sulfate attachment

R:Hesse, L.; Behner, D.; Masters, C.L.; Multhaup, G.

FEBS Lett. 349, 109-116, 1994

A:Title: The beta-A4 amyloid precursor protein binding to copper.

A:Reference number: S46251; MUID:94320627

A:Accession: A39820

A>Status: preliminary

A:Molecule type: protein

A:Residues: 18-32 <POT>

A:Experimental source: brain

C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein

F:625-648/Domain: transmembrane #status predicted <TAM>

OY 1 EISEVKMDAE 10
 |||||||||
 Db 590 EISEVKMDAE 599

Query Match 100.0%; Score 47; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5

QRI004 Alzheimer's disease amyloid beta protein precursor [validated] - human

N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor xia inh

N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascu

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000

C:Accession: S02260; S05194; A32277; A35260; A35486; I39452; I39453; I59562;

4668; A28583; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S38252;

R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;

Nucleic Acids Res. 17, 517-522, 1989

A:Title: The PrEA4(695) precursor protein of Alzheimer's disease A4 amyloid is encode

A:Reference number: S02260; MUID:89128427

A:Accession: S02260

A:Molecule type: DNA

A:Residues: 1-288, 'V', 365-770 <LEM1>

A:Cross-references: EMBL:X13466

R:Lemaire, H.G.

submitted to the EMBL Data Library, November 1988

A:Reference number: S05194

A:Accession: S05194

A:Molecule type: DNA

A:Residues: 1-75 <LAF>

A:Cross-references: GB:M24546; GB:M24547; NID:9441202; PIDN:AA13654.1; PID:9516074

R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.

Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989

A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila

A:Reference number: A33260; MUID:89392030
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <COH>
A:Cross-references: GB:M9270; NID:q178863; PIDN:AAA51768.1; PID:q178665
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A:Reference number: A35486; MUID:90321224
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PREI>
A:Note: 693-Gln was found in DNA isolated from HCMA-D patients
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
Gene 87, 257-263, 1990
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: 139451; MUID:90236318
A:Accession: 139452
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMF
A:Molecule type: DNA
A:Residues: 1-770 <YOSI>
A:Cross-references: GB:M3112; NID:q178613; PIDN:AAB59502.1; PID:q178616
A:Accession: 139451
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMF
A:Molecule type: DNA
A:Residues: 1-530, QWIMPYIPAFWEAKVGR <YOS2>
A:Cross-references: GB:M34875; NID:q178608; PIDN:AAB59501.1; PID:q178615
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168
A:Contents: annotation; erratum
A:Note: revised physical map for reference 139451
R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A:Reference number: 139453; MUID:90260663
A:Accession: 139453
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LEV>
A:Cross-references: GB:M37896; NID:q178618; PIDN:AAA51727.1; PID:q178620
A:Note: A mutation with 693-Gln is presented
R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheim
A:Reference number: 159562; MUID:92022553
A:Accession: 159562
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: GB:S57665; NID:q236720; PIDN:AAB19991.1; PID:q236721
R:Kamino, K.; Orr, H.T.; Payami, H.; Wajsmann, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukul, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A:Reference number: A44017; MUID:99033397
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <RAMI>
A:Cross-references: GB:S45133; NID:q257377; PIDN:AAB23645.1; PID:q257378
A:Experimental source: familial Alzheimer disease family SB
A:Note: sequence extracted from NCBI backbone (NCBIP:115376)
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac
A:Reference number: A03134; MUID:87144572

A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: GB:Y00264; NID:q28525; PIDN:CAA68374.1; PID:q28526
A:Note: alternative splice form App(695)
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascula
A:Reference number: A29030; MUID:87231971
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: GB:M6765; NID:q178539; PIDN:AAA51722.1; PID:q178540
A:Note: the authors translated the codon GAG for residue 647 as Asp
R:Goldhaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amylo
A:Reference number: A47584; MUID:87120328
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: GB:M15533; NID:q178706; PIDN:AAA35540.1; PID:q178707
A:Experimental source: brain
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van
Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near
A:Reference number: A47585; MUID:87120329
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TRAN1>
A:Cross-references: GB:M15532; NID:q177957; PIDN:AAA51564.1; PID:q177958
R:Dyrks, T.; Weidemann, A.; Mulhapp, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mue
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 p
A:Reference number: S02638; MUID:86296437
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
R:Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; N
Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc
A:Reference number: S00707; MUID:8612640
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TRAN2>
A:Cross-references: EMBL:X06982; NID:q28817; PIDN:CAA30042.1; PID:q28812
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form App(751)
R:Ponte, P.; Gonzalez-Nemitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.;
Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inh
A:Reference number: S00925; MUID:8812639
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: GB:X06989; EMBL:Y00297; NID:q28720; PIDN:CAA30050.1; PID:q28721
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi
A:Reference number: A38949; MUID:8812641
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: GB:X06981; NID:q28816; PIDN:CAA30041.1; PID:q28811
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form App(770)
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre
A:Reference number: A30320
A:Accession: A30320
A:Status: not compared with conceptual translation

A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-770 <VIT1>
 A:Accession: B30320
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 122-288, 'V', 365-770 <VIT2>
 A:Accession: C30320
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 606-770 <VIT3>
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A:Title: Molecular cloning of amyloid CDNA derived from mRNA of the Alzheimer disease
 A:Reference number: A31087; MUID:88124954
 A:Accession: A31087
 A:Molecule type: mRNA
 A:Residues: 507-770 <ZAI>
 A:Cross-references: GB:M18724; NID:g178572; PIDN:AA51726.1; PID:g178573
 A>Note: The authors translated the codon GAA for residue 559 as Gly, ACC for residue 603
 8 as Val, GTC for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 65
 A>Note: the cited Genbank accession number, J03594, is not in release 101.0
 R:Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther, K.

Query Match
 Best Local Similarity 100.0%; Score 47; DB 1; Length 770;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
 |||||

Db 665 EISEVKMDAE 674

RESULT 6
 JH0773
 Alzheimer's disease amyloid beta protein precursor - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
 C:Accession: JH0773
 R:Okado, H.; Okamoto, H.
 Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
 A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
 A:Reference number: JH0773; MUID:93122227
 A:Accession: JH0773
 A:Molecule type: mRNA
 A:Residues: 1-747 <OKA>
 A:Cross-references: GB:S52417; NID:g263150; PIDN:AA524853.1; PID:g263151
 A:Experimental source: larva
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; amyloid
 F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match
 Best Local Similarity 93.6%; Score 44; DB 2; Length 747;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
 |||||

Db 642 EISEVKMDSE 651

RESULT 7
 S23094
 beta-amyloid protein precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
 C:Accession: S23094
 R:Kojima, S.; Omori, M.
 FEBS Lett. 304, 57-60, 1992
 A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
 A:Reference number: S23094; MUID:92316198
 A:Accession: S23094
 A:Molecule type: protein
 A:Residues: 1-33 <KOU>

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 Query Match
 Best Local Similarity 80.9%; Score 38; DB 2; Length 33;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SEVKMDAE 10
 |||||

Db 1 SEVKMDAE 8

RESULT 8
 E60045
 Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
 C:Species: Ovis sp. (sheep)
 C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C:Accession: E60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
 A:Reference number: A60045; MUID:92017079
 A:Accession: E60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56130
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match
 Best Local Similarity 100.0%; Score 38; DB 2; Length 57;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SEVKMDAE 10
 |||||

Db 1 SEVKMDAE 8

RESULT 9
 F60045
 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
 C:Accession: F60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
 A:Reference number: A60045; MUID:92017079
 A:Accession: F60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match
 Best Local Similarity 80.9%; Score 38; DB 2; Length 57;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SEVKMDAE 10
 |||||

Db 1 SEVKMDAE 8

RESULT 10
 G60045
 Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
 C:Species: Cavia porcellus (guinea pig)
 C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C:Accession: G60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
 A:Reference number: A60045; MUID:92017079

A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein: animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match
Best Local Similarity 100.0%; Score 38; DB 2; Length 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEVKMDAE 10
|||||
Db 1 SEVKMDAE 8

RESULT 11
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: D60045

A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56124
C:Superfamily: Alzheimer's disease amyloid beta protein: animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match
Best Local Similarity 100.0%; Score 38; DB 2; Length 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEVKMDAE 10
|||||
Db 1 SEVKMDAE 8

RESULT 12
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: A60045

A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein: animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match
Best Local Similarity 100.0%; Score 38; DB 2; Length 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEVKMDAE 10
|||||
Db 1 SEVKMDAE 8

RESULT 13
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: B60045

A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56128; NID:92165; PIDN:CA39593.1; PID:92166
C:Superfamily: Alzheimer's disease amyloid beta protein: animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match
Best Local Similarity 100.0%; Score 38; DB 2; Length 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEVKMDAE 10
|||||
Db 1 SEVKMDAE 8

RESULT 14
G84245
NADH dehydrogenase [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: G84245

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Edhardt, H.; Lowe, T.M.;
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483
A:Accession: G84245

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-389 <STO>
A:Cross-references: GB:AE004437; NID:910580455; PIDN:AA619331.1; GSPDB:GN00138
C:Genetics:
A:Gene: yj1D

Query Match
Best Local Similarity 70.0%; Score 36; DB 1; Length 261;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
||:|||||
Db 251 EISDVEMDAE 260

RESULT 15
C64572
conserved hypothetical protein HP0419 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jun-2000
C:Accession: C64572

R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Sutton, R.A.; Sutton, G.G.; Fleischmann, R
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKe
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpe, P.D.; Smith, H.O.; Fraser
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467
A:Accession: C64572

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-261 <TOM>
A:Cross-references: GB:AE000557; GB:AE000511; NID:92313514; PIDN:AA007484.1; PID:9231
F;36-161/Domain: bioc homology <BIOC>

Query Match
Best Local Similarity 76.6%; Score 36; DB 1; Length 261;

QY 76.6%; Score 36; DB 1; Length 261;

Db 1 SEVKMDAE 8

RESULT 13
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

Query Match
Best Local Similarity 100.0%; Score 38; DB 2; Length 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 60.0%; Pred. No. 7.7;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
|||::|::|
Db 29 EISQIKIDSE 38

Search completed: October 29, 2002, 10:30:58
Job time : 11.4286 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:36 ; Search time 5 Seconds

(without alignments)
77.439 Million cell updates/sec

Title: US-09-580-018-2

Perfect score: 47

Sequence: 1 EISEVKMDAE-10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SWISSPROT-40*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	751	1 A4_SAISC	Q95241 salmirti sci
2	47	100.0	770	1 A4_HUMAN	P05067 homo sapien
3	47	100.0	770	1 A4_MOUSE	P12023 mus musculu
4	47	100.0	770	1 A4_RAT	P08592 rattus norv
5	42	89.4	58	1 A4_CANFA	Q28280 canis fami
6	42	89.4	59	1 A4_BOVIN	Q28053 bos tauris
7	38	80.9	57	1 A4_PIG	Q29023 sus scrofa
8	38	80.9	57	1 A4_URSWA	Q29149 ursus marit
9	38	80.9	58	1 A4_RABIT	Q28748 oryctolagus
10	38	80.9	58	1 A4_SHEEP	Q28757 ovis aries
11	34	72.3	589	1 HIBN_XENLA	P06180 xenopus lae
12	33	70.2	419	1 A47K_PSECU	P31521 pseudomona
13	33	70.2	800	1 PARC_STRAU	P50073 staphylococ
14	32	68.1	705	1 YNP9_CAEEL	P34562 caenorhabdi
15	32	68.1	793	1 TL21_CHICK	Q9dd78 gallus gall
16	31	66.0	178	1 YJGA_HAEIN	P45076 haemophilus
17	31	66.0	183	1 YJGA_ECOLI	P26650 escherichia
18	31	66.0	214	1 SC14_SCHCO	P35795 schizophyll
19	31	66.0	227	1 G786_HUMAN	Q92520 homo sapien
20	31	66.0	249	1 YXEO_BKCSU	P54554 bacillus su
21	31	66.0	334	1 HBP2_HUMAN	O75031 homo sapien
22	31	66.0	347	1 SNXG_HUMAN	P57768 homo sapien
23	31	66.0	451	1 HEMN_PARDE	O51676 paracoccus
24	31	66.0	993	1 RPNI_YEAST	P38764 saccharomyc
25	31	66.0	1012	1 CX05_HUMAN	O75665 homo sapien
26	31	66.0	1682	1 MSP1_PLAF3	P19598 plasmodium
27	30	63.8	80	1 EX75_PSEAE	O9hwy5 pseudomona
28	30	63.8	127	1 ILBP_PIG	P10289 sus scrofa
29	30	63.8	296	1 H1S1_YARLI	O99145 yarrowia 11
30	30	63.8	304	1 PH85_KIULA	O92241 kluyveromyc
31	30	63.8	305	1 PH85_YEAST	P17157 saccharomyc
32	30	63.8	332	1 MDHC_BETVU	O9sm18 beta vulgar
33	30	63.8	464	1 SPNS_SCHPO	P48010 schizosaccha

34	30	63.8	483	1 YC02_YEAST	P25632 saccharomyc
35	30	63.8	488	1 GAB4_CHICK	P24045 gallus gall
36	30	63.8	538	1 THSH_METTH	O26885 methanobact
37	30	63.8	554	1 NUSM_API11	P34855 apis mellif
38	30	63.8	656	1 V091_FOWPV	O72896 fowlpox vir
39	30	63.8	704	1 HS85_TRYCR	P06660 trypanosoma
40	30	63.8	722	1 MESD_LEUME	Q10418 leucocostoc
41	30	63.8	763	1 DPO3_SULSH	O05706 sulfolobus
42	30	63.8	789	1 V1B4_AGR79	P05353 agrobacteri
43	30	63.8	856	1 CLPB_HELPJ	O9znh1 helicobacte
44	30	63.8	856	1 CLPB_HELPJ	P71404 helicobacte
45	30	63.8	1514	1 NX1A_RAT	O63372 rattus norv

ALIGNMENTS

```

RESULT 1
A4_SAISC ID A4_SAISC STANDARD; PRT; 751 AA.
AC Q95241:
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-
DE amyloid protein (beta-Ap) (A-beta)].
GN App.
OS Salmirti sciureus (common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Salmirti.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy E., Amorim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with
RT cerebral amyloid angiopathy.";
RL Neurobiol. Aging 16:805-808(1995).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPT1/KUNITZ INHIBITOR DOMAIN.
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: S81024; AAD14347.1; -.
DR HSSP: P05067; IAPP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPT1.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPT1; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPT1_KUNITZ_1; 1.
DR PROSITE: PS0279; BPT1_KUNITZ_2; 1.

```

KW Glycoprotein; Amyloid; Neurope; Transmembrane; Alternative splicing;
 KM Signal: Serine protease inhibitor.
 FT CHAIN 1 17 BY SIMILARITY.
 FT CHAIN 18 751 A4 PROTEIN.
 FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
 FT TRASMEN 681 704 POTENTIAL.
 FT DOMAIN 705 751 CYTOSOLASMIC (POTENTIAL).
 FT DOMAIN 287 345 BPT/KUNITZ INHIBITOR.
 FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
 FT ACT-SITE 301 302 REACTIVE BOND.
 FT DISULFID 291 341 BY SIMILARITY.
 FT DISULFID 300 324 BY SIMILARITY.
 FT DISULFID 316 337 BY SIMILARITY.
 FT CAROHND 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CAROHND 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).
 SQ SEQUENCE 751 AA; 84893 MW; 6C3EA31089569049 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 751;
 Best Local Similarity 100.0%; Pred. No. 0.085;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EISEVMDAE 10
 |||||||||
 Db 646 EISEVMDAE 655

RESULT 2
 A4_HUMAN STANDARD; PRT; 770 AA.
 ID A4_HUMAN
 AC P05067; P09000; Q16011;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II)
 DE (PN-II) (APP) [contains: Beta-amyloid protein (beta-Ap4) (A-beta)].
 GN APP OR A4 OR CVAP OR A4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=87144572; PubMed=2881207;
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
 RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
 RT cell-surface receptor".
 RL Nature 325:733-736(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA MEDLINE=88122639; PubMed=2893289;
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
 RA Corell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine
 RT proteinase inhibitors".
 RL Nature 331:525-527(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=89128427; PubMed=2873775;
 RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The PREAM(695) precursor protein of Alzheimer's disease A4 amyloid
 RT is encoded by 16 exons".
 RL Nucleic Acids Res. 17:517-522(1989).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=97263807; PubMed=9108164;
 RA Hattori M., Tsukihara F., Furuhata Y., Tanahashi H., Hirose M.,
 RA Saio M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for

RT sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [5]
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
 RX MEDLINE=88122640; PubMed=2893290;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease".
 RL Nature 331:528-530(1988).
 RN [6]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity".
 RL Nature 331:530-532(1988).
 RN [7]
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides".
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [8]
 RP SEQUENCE OF 507-770 FROM N.A.
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex".
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [9]
 RP SEQUENCE OF 672-681.
 RX MEDLINE=88035004; PubMed=3312495;
 RA Padridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tountelliotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels".
 RL J. Neurochem. 49:1394-1401(1987).
 RN [10]
 RP SEQUENCE OF 739-770 FROM N.A.
 RX MEDLINE=90236318; PubMed=2110105;
 RA Yoshikawa S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene".
 RL Gene 87:257-263(1990).
 RN [11]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Liver;
 RA MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABP)
 RT encodes a 95-kDa polypeptide".
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [12]
 RP SEQUENCE OF 18-50.
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts".
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [13]
 RP IDENTITY OF APP WITH NEXIN-II.
 RX MEDLINE=89384866; PubMed=2506449;
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
 RA Sinha S.;
 RT "The secreted form of the Alzheimer's amyloid precursor protein with
 RT the Kunitz domain is protease nexin-II".
 RL Nature 341:144-147(1989).
 RN [14]

RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RX MEDLINE=9021252; PubMed=1969731;
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
 RT "Protease-specificity of kunitz inhibitor domain of Alzheimer's
 RT disease amyloid protein precursor.";
 RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
 RN [15]
 RP COMPLEX WITH G(O).
 RX MEDLINE=9318965; PubMed=8446172;
 RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 RT protein G(O)."
 RL Nature 362:75-79(1993).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
 RX MEDLINE=99215582; PubMed=10201399;
 RA Rosjohn J., Cappai R., Fell S.C., Henry A., McKinstiry W.J.,
 RA Galatis D., Heese L., Muthaup G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RT "Crystal structure of the N-terminal, growth factor-like domain of
 RT Alzheimer amyloid precursor protein.";
 RL Nat. Struct. Biol. 6:327-331(1999).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
 RX MEDLINE=91104913; PubMed=2125487;
 RA Hynes T.R., Randall M., Kennedy L.A., Eigenbrodt C., Kosiakof A.A.;
 RT "X-ray crystal structure of the protease inhibitor domain of
 RT Alzheimer's amyloid beta-protein precursor.";
 RL Biochemistry 29:10018-10022(1990).
 RN [18]
 RP STRUCTURE BY NMR OF 289-344.
 RX MEDLINE=92031488; PubMed=1718421;
 RA Heald S.L., Tilton R.F., Jr., Hammond L.S., Lee A., Bayney R.M.,
 RA Kamaek M.E., Rambhadraran T.V., Dreyer R.N., Davis G., Unterbeck A.,
 RA Tamburini P.P.;
 RT "Sequential NMR resonance assignment and structure determination of
 RT the kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
 RT precursor protein.";
 RL Biochemistry 30:10467-10478(1991).
 RN [19]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=94281210; PubMed=7516706;
 RA Talafous J., Marcinkowski K.J., Klopman G., Zagorski M.G.;
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
 RL Biochemistry 33:7788-7796(1994).
 RN [20]
 RP STRUCTURE BY NMR OF 696-706.
 RX MEDLINE=97128622; PubMed=8973180;
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
 RT membrane-mimicking environment.";
 RL Biochemistry 35:16094-16104(1996).
 RN [21]
 RP STRUCTURE BY NMR OF 672-711.
 RX MEDLINE=98359783; PubMed=9693002;
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle
 RT environment. Is the membrane-spanning domain where we think it is?";
 RL Biochemistry 37:11064-11077(1998).
 RN [22]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=20400066; PubMed=10940222;
 RA Poulsen S.-A., Watson A.A., Craik D.J.;
 RT "Solution structures in aqueous SDS micelles of two amyloid beta
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
 RT site.";
 RL J. Struct. Biol. 130:142-152(2000).
 RN [23]
 RP STRUCTURE BY NMR OF 681-706.
 RX MEDLINE=20400065; PubMed=10940221;
 RA Zhang S., Iwata K., Lachemann M.J., Peng J.W., Li S., Stimson E.R.,
 RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;

RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in
 RT water.";
 RL J. Struct. Biol. 130:130-141(2000).
 RN [24]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
 RX MEDLINE=88296437; PubMed=2900137;
 RA Dykes T., Weidemann A., Muthaup G., Salbaum J.M., Lemaire H.-G.,
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
 RT "Identification, transmembrane orientation and biogenesis of the
 RT amyloid A4 precursor of Alzheimer's disease.";
 OY 1 EISEVKMDAE 10 100.0%; Score 47; DB 1; Length 770;
 DB 665 EISEVKMDAE 674 Best Local Similarity 100.0%; Pred. No. 0.087;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 3
 AA_MOUSE STANDARD; PRT: 770 AA.
 ID A4_MOUSE
 AC P12023;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog precursor
 DE (Amyloidogenic glycoprotein) (M6).
 GN App.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC STRAIN-BALB/C; TISSUE=Brain;
 RX MEDLINE=92096456; PubMed=1756177;
 RA de Strooper B., van Leeuwen F., van den Bergh H.;
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse
 RT is closer related to its human homolog than previously reported.";
 RL Biochim. Biophys. Acta 1129:141-143(1991).
 RN [2]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=88106489; PubMed=3322280;
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 RT protein precursor.";
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
 RN [3]
 RP REVISIONS.
 RA Yamada T.;
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE=89345111; PubMed=2569710;
 RA Fukuchi K., Martin G.M., Deep S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of Mus domesticus.";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [5]
 RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE=92209998; PubMed=1555768;
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
 RA Sakai Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RL Gene 112:189-195(1992).
 RN [6]
 RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Kidney;

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RX MEDLINE=89149813; PubMed=2493250;
RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RT for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor."
RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
CC LIVER.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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CC -----
DR EMBL: X59379; -; NOT_ANNOTATED_CDS.
DR EMBL: M18373; AAA37139.1; -.
DR EMBL: X15210; CAA33280.1; -.
DR EMBL: D10603; BAA01456.1; -.
DR EMBL: M24397; AAA39929.1; -.
DR PIR: A27485; A27485.
DR PIR: S04855; S04855.
DR PIR: S19727; S19727.
DR HSSP: P05067; IQCM.
DR MGD: MGI:88059; IQCM.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00739; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
DR GlycoProfile: Amyloid; Neurone; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor;
FT SIGNAL 1 17
FT CHAIN 18 770
FT FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT FT EXTRACELLULAR (POTENTIAL).
FT FT POTENTIAL.
FT FT CYTOPLASMIC (POTENTIAL).
FT FT EQUIVALENT OF BETA-AMYLOID PROTEIN.
FT FT BPTI/KUNITZ INHIBITOR.
FT FT CLATHRIN-BINDING (BY SIMILARITY).
FT FT BY SIMILARITY.
FT FT BY SIMILARITY.
FT FT BY SIMILARITY.
FT FT BY SIMILARITY.
FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 571 571 E -> V (IN ISOFORM APP(695)).
FT FT VARSPLIC 289 289 E -> V (IN ISOFORM APP(695)).
FT FT VARSPLIC 290 364 MISSING (IN ISOFORM APP(751)).
FT FT VARSPLIC 346 380 MISSING (IN ISOFORM APP(751)).
FT FT SEQUENCE 770 AA; 86752 MW; 2650DE0890CAFA7A CRC64;
Query Match 100.0%; Score 47; DB 1; Length 770;

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Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EISEVKMDAE 10
Db 665 EISEVKMDAE 674
RESULT 4
ID A4_RAT STANDARD: PRT; 770 AA.
AC P08592;
DT 01-DEC-1988 (rel. 08, Created)
DT 16-OCT-1992 (rel. 24, Last sequence update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (AG).
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact."
RN EMBL J. 7:1365-1370(1988).
[2]
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4."
RL Nucleic Acids Res. 17:2130-2130(1989).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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CC -----
DR EMBL: X07648; CAA30488.1; -.
DR EMBL: X14066; CAA32229.1; -.
DR PIR: S00550; S00550.
DR PIR: S03607; S03607.
DR HSSP: P05067; IAAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00739; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.

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QY      2 ISEVKMDAE 10
      1 ISEVKMDAE 9

RESULT 7
AA_PIG
ID AA_PIG          STANDARD:      PRT:      57 AA.
AC Q23023;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-ApP) (A-beta)] (Fragment).
GN APP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;

RN
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: X56127; CAA39592.1; -
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 48
FT DOMAIN <1 33 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).
FT NON_TER 57 57 POTENTIAL.
SQ SEQUENCE 57 AA: 6172 MW: 84209D88EBA82DFA CRC64;

Query Match 80.9%; Score 38; DB 1; Length 57;
Best Local Similarity 100.0%; Pred No. 0.37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SEVKMDAE 10
      1 SEVKMDAE 8

RESULT 8
AA_URSMA
ID AA_URSMA          STANDARD:      PRT:      57 AA.
AC Q23149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid

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DE protein (Beta-ApP) (A-beta)] (Fragment).
GN APP.
OS Ursus maritimus (Polar bear) (Thalartos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;

RN
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: X56128; CAA39593.1; -
DR HSSP: P05067; 1AM4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 48
FT DOMAIN <1 33 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).
FT NON_TER 57 57 POTENTIAL.
SQ SEQUENCE 57 AA: 6172 MW: 84209D88EBA82DFA CRC64;

Query Match 80.9%; Score 38; DB 1; Length 57;
Best Local Similarity 100.0%; Pred No. 0.37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SEVKMDAE 10
      1 SEVKMDAE 8

RESULT 9
AA_RABIT
ID AA_RABIT          STANDARD:      PRT:      58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-ApP) (A-beta)] (Fragment).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;

RN
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";

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RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -----
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -----
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CC -----
DR EMBL: X56129; CAA39594.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D8EBA82D CRC64;

Query Match
Best Local Similarity 100.0%; Score 38; DB 1; Length 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEVKMDAE 10
Db 1 SEVKMDAE 8

RESULT 10
A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-Ap) (A-beta)] (Fragment).
GN A4P.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnson E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -----
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -----
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: X56130; CAA39595.1; -.
DR HSSP: P05067; 1AML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D8EBA82D CRC64;

Query Match
Best Local Similarity 100.0%; Score 38; DB 1; Length 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEVKMDAE 10
Db 1 SEVKMDAE 8

RESULT 11
H1BN_XENLA STANDARD; PRT; 589 AA.
ID H1BN_XENLA
AC P06180;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Histone-binding protein H1/N2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Oocyte;
RX MEDLINE=87161764; PubMed=3549279;
RA Kleinschmidt J.A., Dingwall C., Maier G., Franke W.W.;
RT "Molecular characterization of a karyophilic, histone-binding
RT protein: cDNA cloning, amino acid sequence and expression of nuclear
RT protein H1/N2 of Xenopus laevis."
RL EMBO J. 5:3547-3552(1986).
CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN NUCLEOSOME ASSEMBLY. IT
CC IS BOUND TO H3 AND H4 IN THE ABSENCE OF DNA, BUT RELEASED FROM
CC H3 AND H4 IN THE PRESENCE OF DNA.
CC -----
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -----
CC -1- SIMILARITY: WITH RABBIT NUCLEAR AUTOANTIGENIC SPERM PROTEIN.
CC -----
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CC -----
DR EMBL: X04712; CAA28419.1; -.
DR PIR: A25680; A25680.
DR InterPro: IPR001440; TPR.
DR Pfam: PF00515; TPR; 3.
KW Nuclear protein; Chromosomal protein.
FT INT_MET 0
FT DOMAIN 107 118 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 289 325 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 530 536 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ SEQUENCE 589 AA; 64897 MW; AC28927B4D4E245B CRC64;

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Query Match      72.3%; Score 34; DB 1; Length 589;
Best Local Similarity 60.0%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
   1111111111
Db 259 EVAEEKMDSE 268

RESULT 12
P47K.PSECL      STANDARD:      PRT: 419 AA.
ID P47K.PSECL
AC P31521;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 47 kDa protein (P47K).
OS Pseudomonas chlororaphis (Pseudomonas aureofaciens).
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=333;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-B23;
RX MEDLINE-91193202; PubMed-2013568;
RA Nishiyama M., Horinouchi S., Kobayashi M., Nagasawa T., Yamada H.,
RA Bepu T.;
RT "Cloning and characterization of genes responsible for metabolism of
RT nitrile compounds from Pseudomonas chlororaphis B23."
RL J. Bacteriol. 173:2465-2472(1991).
CC -I- FUNCTION: THE PRESENCE OF P47K IS CRITICAL FOR THE EXPRESSION
CC OF THE NITRILE HYDRATASE GENES. MAY STABILIZE OR ACTIVATE THE
CC NITRILE HYDRATASE PROTEINS.
CC -----
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CC -----
DR EMBL: D90216; BAA14247.1; -.
DR PIR: D42725; D42725.
DR InterPro: IPR003495; COBW.
DR Pfam: PF02492; COBW; 1.
SQ SEQUENCE 419 AA; 4666 MW; F5113800E27FF0C CRC64;

Query Match      70.2%; Score 33; DB 1; Length 419;
Best Local Similarity 60.0%; Pred. No. 30;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
   1111111111
Db 45 DMEVNLDAE 54

RESULT 13
PARC.STAAU      STANDARD:      PRT: 800 AA.
ID PARC.STAAU
AC P50073; P95682; P95683;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Topoisomerase IV subunit A (EC 5.99.1.-).
GN PARC OR GRLA.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-FDA 574;

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RX MEDLINE=95089700; PubMed=7997176;
RA Ferrero L., Cameron B., Manse B., Lagneaux D., Crouzet J.,
RA Fereccon A., Blanche F.;
RT "Cloning and primary structure of Staphylococcus aureus DNA
RT topoisomerase IV: a primary target of fluoroquinolones."
RL Mol. Microbiol. 13:641-653(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-KMP9, AND RM4220;
RX MEDLINE=96300529; PubMed=8723458;
RA Yamagishi J., Kojima T., Oyama Y., Fujimoto K., Hattori H.,
RA Nakamura S., Inoue M.;
RT "Alterations in the DNA topoisomerase IV grlA gene responsible for
RT quinolone resistance in Staphylococcus aureus."
RL Antimicrob. Agents Chemother. 40:1157-1163(1996).
RN [3]
RP MUTAGENESIS.
RC STRAIN-RM4220;
RX MEDLINE=96104899; PubMed=7492103;
RA Ferrero L., Cameron B., Crouzet J.;
RT "Analysis of gyra and grlA mutations in stepwise-selected
RT ciprofloxacin-resistant mutants of Staphylococcus aureus."
RL Antimicrob. Agents Chemother. 39:1554-1556(1995).
CC -I- FUNCTION: TOPOISOMERASE IV IS ESSENTIAL FOR CHROMOSOME
CC SEGREGATION. IT HAS RELAXATION OF SUPERCOILED DNA ACTIVITY.
CC PERFORMS THE DECATENATION EVENTS REQUIRED DURING THE REPLICATION
CC OF A CIRCULAR DNA MOLECULE (BY SIMILARITY).
CC -I- SUBUNIT: COMPOSED OF TWO SUBUNITS: GRlA AND GRlB.
CC -I- SIMILARITY: STRONG, WITH THE A SUBUNIT OF GRlAS.
CC -----
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CC -----
DR EMBL: L25288; AAA53116.1; -.
DR EMBL: D67074; BAA11085.1; -.
DR EMBL: D67075; BAA11087.1; -.
DR HSSP: P09097; 1AB4.
DR InterPro: IPR002205; DNA_topoisoIV.
DR Pfam: PF00521; DNA_topoisoIV; 1.
DR SMART: SM00434; TOP4c; 1.
KW Topoisomerase; Isomerase; DNA-binding; Antibiotic resistance.
FT ACT_SITE 119 119
FT VARIANT 410 410
FT MOTAGEN 80 80
FT MOTAGEN 84 84
FT CONFLICT 267 267
FT CONFLICT 567 567
FT CONFLICT 594 594
FT CONFLICT 688 688
SQ SEQUENCE 800 AA; 90997 MW; ABE927368475D87 CRC64;

Query Match      70.2%; Score 33; DB 1; Length 800;
Best Local Similarity 60.0%; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
   1111111111
Db 486 EIEIKIKDKE 495

RESULT 14
YNP9.CAEEL      STANDARD:      PRT: 705 AA.
ID YNP9.CAEEL
AC P34562;
DT 01-FEB-1994 (Rel. 28, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Hypothetical 80.6 kDa protein T0565.9 in chromosome III.

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GN T05G5.9.
 OC Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloterinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Caxton M., Dear S., Du Z., Durbin R., Pavello A., Fraser A.,
 RA Ralton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
 RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
 RA Woldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 RN [2]
 RP REVISIONS.
 RA Durbin R.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC -----
 CC EMBL: Z27079; CAAB1596.1; -
 DR PIR: S41009; S41009
 DR Wormpep: T05G5.9; CE21153.
 DR InterPro: IPR000237; GRIP.
 DR Pfam: PF01465; GRIP; 1.
 KW Hypothetical protein; Coiled coil.
 FT DOMAIN 75 137 COILED COIL (POTENTIAL).
 FT DOMAIN 160 509 COILED COIL (POTENTIAL).
 FT DOMAIN 562 641 COILED COIL (POTENTIAL).
 SQ SEQUENCE 705 AA; 80637 MW; 9EB9873F5FC04966 CRC64;
 OY 1 EISEVKKDAE 10
 Db 108 ELEGVKKDAE 117
 RESULT 15
 TL21-CHICK STANDARD; PRT; 793 AA.
 AC Q9DD78;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Toll-like receptor 2 type 1 precursor.
 GN TLR2-1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;

EX PubMed=11590137;
 RA Fukui A., Inoue N., Matsumoto M., Nomura M., Yamada K., Matsuda Y.,
 RA Toyoshima K., Seya T.;
 RT "Molecular cloning and functional characterization of chicken
 RT Toll-like receptors. A single chicken Toll covers multiple molecular
 RT patterns";
 RL J. Biol. Chem. 276:47143-47149(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Takahashi T.;
 RT "Molecular cloning and expression analysis of the chick Toll-like
 RT receptor 2 in embryonic ventricular myocytes";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Participates in the innate immune response to microbial
 CC agents. Acts via MyD88 and TRAF6, leading to NF-kappa-B
 CC activation, cytokine secretion and the inflammatory response (By
 CC similarity). Does not respond to LPS and responds with less
 CC ability than TLR2-2 to mycoplasma macrophage-activating
 CC lipopeptide-2kd (MALP-2).
 CC -1- SUBUNIT: Binds MyD88 via their respective TIR domains. Binds TLR6
 CC via their respective extracellular domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- TISSUE SPECIFICITY: Highly expressed in ovary. Detected at lower
 CC levels in heart, lung, gizzard and testis.
 CC -1- PTM: N-glycosylated. TLR2-1 is more heavily glycosylated than
 CC TLR2-2.
 CC -1- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 TIR DOMAIN
 CC -1- SIMILARITY: CONTAINS 13 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC -----
 CC EMBL: AB050005; BAB16843.1; -
 DR EMBL: AB046119; BAB16113.2; -
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003592; LRR_out.
 DR InterPro: IPR003591; LRR_typ.
 DR InterPro: IPR000157; TIR.
 DR Pfam: PF00360; LRR; 4.
 DR Pfam: PF01463; LRRCT; 1.
 DR Pfam: PF01582; TIR; 1.
 DR PRINTS: PR00019; LEURICRPT.
 DR SMART: SM00370; LRR; 4.
 DR SMART: SM00082; LRRCT; 1.
 DR SMART: SM00369; LRR_TYP; 6.
 DR SMART: SM00255; TIR; 1.
 DR PROSITE: PS50104; TIR; 1.
 KW Receptor; Immune response; Inflammatory response; Signal;
 KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
 FT SIGNAL 1 25
 FT CHAIN 26 793
 FT DOMAIN 26 597
 FT TRANSMEM 598 618
 FT DOMAIN 619 793
 FT REPEAT 62 85
 FT REPEAT 86 109
 FT REPEAT 111 133
 FT REPEAT 135 158
 FT REPEAT 159 182
 FT REPEAT 184 206
 FT REPEAT 206 266
 FT REPEAT 344 370
 FT REPEAT 395 419
 FT REPEAT 421 445
 FT REPEAT 447 465
 FT REPEAT 466 485
 FT REPEAT 486 509
 FT REPEAT 486 509
 LRR 1.
 LRR 2.
 LRR 3.
 LRR 4.
 LRR 5.
 LRR 6.
 LRR 7.
 LRR 8.
 LRR 9.
 LRR 10.
 LRR 11.
 LRR 12.
 TOLL-LIKE RECEPTOR 2 TYPE 1.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 POTENTIAL.

FT REPEAT 511 530 LRR 13.
FT DOMAIN 648 793 TIR.
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 793 AA: 90766 MW: 2Bf659D9305D4562 CRC64:

Query Match 58.18; Score 32; DB 1; Length 793;

Best Local Similarity 50.08; Pred. No. 91;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10

DB 238 EVREIKLDIE 247

Search completed: October 29, 2002, 10:27:26
Job time : 7 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:11 ; Search time 18 Seconds
(without alignments)
96.108 Million cell updates/sec

Title: US-09-580-018-2
Perfect score: 47
Sequence: 1 EISEVKMDAE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum Db seq length: 0
Maximum Db seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_19:*

1: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	79	11	O35463
2	47	100.0	82	4	P78438
3	47	100.0	82	4	O16014
4	47	100.0	82	4	O16019
5	47	100.0	82	4	O16020
6	47	100.0	607	11	O99K32
7	47	100.0	695	6	O95KN7
8	47	100.0	695	11	P97487
9	47	100.0	695	11	O60496
10	47	100.0	770	6	O9TU10
11	46	97.9	534	13	O93296
12	46	97.9	569	13	O9PVL1
13	46	97.9	695	13	O9DCJ8
14	46	97.9	751	13	O9DCJ7
15	44	93.6	693	13	O98SG0
16	44	93.6	695	13	O98SF9

17	44	93.6	747	13	O91963	O91963 xenopus. ap
18	38	80.9	389	17	O9HR27	O9hr27 halobacteri
19	36	76.6	261	16	O25173	O25173 helicobacte
20	36	76.6	261	16	O9ZKH1	O9zkh1 helicobacte
21	35	74.5	818	16	O9ZC65	O9zc65 listeria in
22	34	72.3	141	2	O44749	O44749 borrelia bu
23	34	72.3	141	2	O44784	O44784 borrelia bu
24	34	72.3	141	2	O9R3H3	O9r3h3 borrelia bu
25	34	72.3	141	2	O9R9H8	O9r9h8 borrelia bu
26	34	72.3	141	2	O9S0J3	O9s0j3 borrelia bu
27	34	72.3	141	2	O9S0A9	O9s0a9 borrelia bu
28	34	72.3	141	2	O9S037	O9s037 borrelia bu
29	34	72.3	141	2	O9R2Y5	O9r2y5 borrelia bu
30	34	72.3	141	2	O86117	O86117 borrelia bu
31	34	72.3	141	2	O07496	O07496 borrelia bu
32	34	72.3	141	2	O44779	O44779 borrelia bu
33	34	72.3	141	2	O44788	O44788 borrelia bu
34	34	72.3	321	3	O01213	O01213 mucor muced
35	34	72.3	869	5	O9V6T0	O9v6t0 drosophila
36	34	72.3	1378	5	O45075	O45075 caenorhabdi
37	33	70.2	63	16	O9A063	O9a063 streptococc
38	33	70.2	289	5	O19813	O19813 caenorhabdi
39	33	70.2	324	12	O9Q8M9	O9q8m9 myxoma viru
40	33	70.2	370	10	O9LYK0	O9lyk0 arabidopsis
41	33	70.2	626	2	O56633	O56633 vibrio chol
42	33	70.2	626	2	O9ACW8	O9acw8 vibrio chol
43	33	70.2	626	16	O9KT07	O9kt07 vibrio chol
44	33	70.2	699	13	O57394	O57394 narke japon
45	33	70.2	743	10	O9SLB2	O9slb2 arabidopsis

ALIGNMENTS

RESULT 1

ID O35463 PRELIMINARY; PRT; 79 AA.

AC O35463;

DT 01-JAN-1998 (TREMBLrel. 05, created)

DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).

GN BETA APP.

OS Cricetus griseus (Chinese hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.

OX NCBI_TaxID=10029;

RN [1]

RP SEQUENCE FROM N.A.

RA Sambamurti K., Pinnix I., Gandhi S.;

RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF030413; AAB86608.1; -.

DR HSSP: P05067; 1BA4.

FT NON_TER 1 1

FT NON_TER 79 79

SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match 100.0%; Score 47; DB 11; Length 79;

Best Local Similarity 100.0%; Pred. No. 0.053;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 1 EISEVKMDAE 10

Db 14 EISEVKMDAE 23

RESULT 2

ID P78438 PRELIMINARY; PRT; 82 AA.

AC P78438;

DT 01-MAY-1997 (TREMBLrel. 03, created)

DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)

```
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [2]
RP SEQUENCE OF 19-48 FROM N.A.
RX MEDLINE=87120329; PubMed=2949367;
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Nave R.L.;
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
RT linkage near the Alzheimer locus.";
RL Science 235:880-884(1987).
RN [3]
RP SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE=93035397; PubMed=1415269;
RA Kamino K., Orr H.T., Payami H., Wajsman E.M., Alonso M.E., Pulst S.M.,
RA Anderson L., O'dahl S., Nemens E., White J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease
RT kindreds for the APP gene region.";
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL: M29270; AAAS1768.1; -.
DR EMBL: M29269; AAAS1768.1; JOINED.
DR EMBL: M15532; AAAS1564.1; -.
DR EMBL: S45136; AAB23646.1; -.
DR HSSP: P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
Db 10 EISEVKMDAE 19

RESULT 3
Q16014 PRELIMINARY; PRT; 82 AA.
ID Q16014;
AC Q16014;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S60721; AAB26263.2; -.
DR HSSP: P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;
```

```
Query Match
Best Local Similarity 100.0%; Score 47; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
Db 11 EISEVKMDAE 20

RESULT 4
Q16019 PRELIMINARY; PRT; 82 AA.
ID Q16019;
AC Q16019;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S61380; AAB26264.2; -.
DR HSSP: P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
Db 11 EISEVKMDAE 20

RESULT 5
Q16020 PRELIMINARY; PRT; 82 AA.
ID Q16020;
AC Q16020;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S61383; AAB26265.2; -.
DR HSSP: P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8882 MW; F534AA5A5ED9230A CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 EISEVKMDAE 10
 1111111111
 DB 11 EISEVKMDAE 20

RESULT 6

ID Q99K32 PRELIMINARY; PRT; 607 AA.
 AC Q99K32;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, last annotation update)
 DE HYPOTHETICAL 68.4 KDA PROTEIN (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MAMMARY TUMOR. MAP-TGF ALPHA MODEL. 7 MONTHS OLD, CROSS
 RC TISSUE=;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC005490; AAH05490.1; -.
 DR HSSP: P05067; IAPP.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI. 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRINTS: PR00759; BASICPTASE.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
 KM Hypothetical protein; Serine protease inhibitor.
 FT NON_TER 1
 SQ SEQUENCE 607 AA; 68391 MW; BFR02214CBA7D172 CRC64;

Query Match 100.0%; Score 47; DB 11; Length 607;
 Best Local Similarity 100.0%; Pred. No. 0.41;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
 1111111111
 DB 502 EISEVKMDAE 511

RESULT 7

ID Q95KN7 PRELIMINARY; PRT; 695 AA.
 AC Q95KN7;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
 DE AMYLOID B-PROTEIN PRECURSOR.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CEREBELLUM;
 RX MEDLINE=91273117; PubMed=1905108;
 RA Podlasky M.B., Tolan D.R., Selkoe D.J.;
 RT "Homology of the amyloid beta protein precursor in monkey and human
 RT supports a primate model for beta amyloidosis in Alzheimer's
 RT disease";
 RL Am. J. Pathol. 138:1423-1435(1991).
 DR EMBL: M58727; AAA36829.1; -.
 FT SIGNAL 1 17 POTENTIAL.

FT CHAIN 597 636 POTENTIAL.
 SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match 100.0%; Score 47; DB 6; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.47;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
 1111111111
 DB 590 EISEVKMDAE 599

RESULT 8

ID P97487 PRELIMINARY; PRT; 695 AA.
 AC P97487; P97942;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
 DE HIPPOCAMPAL AMYLOID PROTEIN.
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SAMP8; TISSUE=HIPPOCAMPUS;
 RA Flood J.F., Kumar V.B., Sasser T., Word I., Morley J.E.;
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 581-662 FROM N.A.
 RC STRAIN=129SV;
 RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capechi M.,
 RA Loring J.F., Goate A.M.;
 RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U84012; AAB41502.1; -.
 DR EMBL: U82624; AAB40919.1; -.
 DR HSSP: P05067; IAPP.
 DR MGD: MGI:88059; APP.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78414 MW; 9A5FBE2ED261236E CRC64;

OY 1 EISEVKMDAE 10
 1111111111
 DB 590 EISEVKMDAE 599

Query Match 100.0%; Score 47; DB 11; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.47;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
 1111111111
 DB 590 EISEVKMDAE 599

RESULT 9

ID Q60496 PRELIMINARY; PRT; 695 AA.
 AC Q60496;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
 DE PUTATIVE AMYLOID PRECURSOR PROTEIN.
 OS Cavia sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
 OX NCBI_TaxID=10143;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=97236426; PubMed=9116031;

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RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing.";
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL; X97631; CAA66230.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 100.0%; Score 47; DB 11; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
Db 590 EISEVKMDAE 599

RESULT 10
Q9TU10 PRELIMINARY; PRT; 770 AA.
AC Q9TU10;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (Pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid precursor protein 770.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032550; BAA84580.1; -.
DR HSSP; P05067; 1AAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5FALD0CB2BC583E CRC64;

Query Match 100.0%; Score 47; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
Db 665 EISEVKMDAE 674

RESULT 11
Q93296 PRELIMINARY; PRT; 534 AA.
AC Q93296;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

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DE AMYLOID PROTEIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL; AF042098; AAC25052.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2B66DAC92 CRC64;

Query Match 97.9%; Score 46; DB 13; Length 534;
Best Local Similarity 90.0%; Pred. No. 0.57;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
Db 429 EISEVKMDAE 438

RESULT 12
Q9PVL1 PRELIMINARY; PRT; 569 AA.
AC Q9PVL1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Coulson E.J., Paliya K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function.";
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12698.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;

Query Match 97.9%; Score 46; DB 13; Length 569;
Best Local Similarity 90.0%; Pred. No. 0.61;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
Db 465 EISEVKMDAE 474

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RESULT 13

Q9DGJ8 PRELIMINARY; PRT; 695 AA.
 ID Q9DGJ8;
 AC Q9DGJ8;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NC NCBL_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolosse A., Sorribas V.;
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 RT isoforms";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF289218; AAC00593.1; -
 DR HSSP: P05067; 1BA4.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match

Best Local Similarity 97.9%; Score 46; DB 13; Length 695;
 Best Local Similarity 90.0%; Pred. No. 0.74;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
 Db 590 EVSEVKMDAE 599

RESULT 14

Q9DGJ7 PRELIMINARY; PRT; 751 AA.
 ID Q9DGJ7;
 AC Q9DGJ7;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NC NCBL_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolosse A., Sorribas V.;
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 RT isoforms";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF289219; AAC00594.1; -
 DR HSSP: P05067; 1BA4.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRINTS: PR00759; BASICPTASE.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor.
 SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 97.9%; Score 46; DB 13; Length 751;
 Best Local Similarity 90.0%; Pred. No. 0.8;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
 Db 646 EVSEVKMDAE 655

RESULT 15

Q98SG0 PRELIMINARY; PRT; 693 AA.
 ID Q98SG0;
 AC Q98SG0;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE BETA-AMYLOID PRECURSOR PROTEIN A.
 GN APP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NC NCBL_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Van den Hurk W.H.;
 RL Thesis (2001), Department of Biological Sciences,
 RL University of Nijmegen, Nijmegen, Netherlands.
 DR EMBL: AJ298150; CAC37193.1; -
 DR HSSP: P05067; 1H23.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 693 AA; 78568 MW; CAFIDF55C1AB653 CRC64;
 POTENTIAL.

Query Match

Best Local Similarity 93.6%; Score 44; DB 13; Length 693;
 Best Local Similarity 90.0%; Pred. No. 1.9;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
 Db 588 EISEVKMDSE 597

Search completed: October 29, 2002, 10:29:38
 Job time : 19.1429 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:56 : Search time 9 Seconds
(without alignments)
27.140 Million cell updates/sec

File: US-09-580-018-2
Perfect score: 47
Sequence: 1 EISEYKMDAE 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*

- 1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/PCTUS.COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	47	100.0	27	1	US-08-141-324-11	Sequence 11, Appl
2	47	100.0	27	1	US-08-541-902-11	Sequence 11, Appl
3	47	100.0	45	1	US-08-462-859A-5	Sequence 5, Appl
4	47	100.0	45	1	US-08-123-659A-5	Sequence 5, Appl
5	47	100.0	45	1	US-08-464-247A-5	Sequence 5, Appl
6	47	100.0	45	1	US-08-464-248A-5	Sequence 5, Appl
7	47	100.0	58	1	US-08-371-930-25	Sequence 25, Appl
8	47	100.0	58	5	PCT-US94-01712-25	Sequence 25, Appl
9	47	100.0	63	1	US-08-462-859A-3	Sequence 3, Appl
10	47	100.0	63	1	US-08-462-859A-4	Sequence 3, Appl
11	47	100.0	63	1	US-08-123-659A-3	Sequence 3, Appl
12	47	100.0	63	1	US-08-123-659A-4	Sequence 3, Appl
13	47	100.0	63	1	US-08-464-247A-3	Sequence 3, Appl
14	47	100.0	63	1	US-08-464-247A-4	Sequence 3, Appl
15	47	100.0	63	1	US-08-464-248A-3	Sequence 3, Appl
16	47	100.0	63	1	US-08-464-248A-4	Sequence 3, Appl
17	47	100.0	152	6	5187153-4	Sequence 4, Appl
18	47	100.0	152	6	5220013-4	Sequence 4, Appl
19	47	100.0	162	6	5223482-4	Sequence 4, Appl
20	47	100.0	264	1	US-07-990-893-5	Sequence 5, Appl
21	47	100.0	487	1	US-08-462-859A-9	Sequence 9, Appl
22	47	100.0	487	1	US-08-123-659A-9	Sequence 9, Appl
23	47	100.0	487	1	US-08-464-247A-9	Sequence 9, Appl
24	47	100.0	487	1	US-08-464-248A-9	Sequence 9, Appl
25	47	100.0	492	1	US-08-462-859A-7	Sequence 7, Appl
26	47	100.0	492	1	US-08-123-659A-7	Sequence 7, Appl
27	47	100.0	492	1	US-08-464-247A-7	Sequence 7, Appl

28	47	100.0	492	1	US-08-464-248A-7	Sequence 7, Appl
29	47	100.0	537	1	US-08-453-552-4	Sequence 4, Appl
30	47	100.0	537	2	US-08-710-637-4	Sequence 4, Appl
31	47	100.0	537	5	PCT-US93-00907-4	Sequence 4, Appl
32	47	100.0	636	1	US-08-371-930-23	Sequence 23, Appl
33	47	100.0	656	5	PCT-US94-01712-23	Sequence 23, Appl
34	47	100.0	676	1	US-08-371-930-24	Sequence 24, Appl
35	47	100.0	676	5	PCT-US94-01712-24	Sequence 24, Appl
36	47	100.0	694	1	US-08-339-152A-18	Sequence 18, Appl
37	47	100.0	694	2	US-08-007-999B-5	Sequence 5, Appl
38	47	100.0	694	2	US-08-689-276A-5	Sequence 5, Appl
39	47	100.0	695	1	US-08-371-930-27	Sequence 27, Appl
40	47	100.0	695	1	US-08-123-702-2	Sequence 2, Appl
41	47	100.0	695	1	US-08-339-152A-30	Sequence 30, Appl
42	47	100.0	695	2	US-08-104-165-1	Sequence 1, Appl
43	47	100.0	695	3	US-08-464-250-1	Sequence 1, Appl
44	47	100.0	695	4	US-08-464-250-1	Sequence 1, Appl
45	47	100.0	695	4	US-09-458-481B-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-141-324-11
Sequence 11, Application us/08141324
Patent No. 5475097

GENERAL INFORMATION:
APPLICANT: TRAVIS, James
APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Nadine
APPLICANT: Pike, Robert N.
TITLE OF INVENTION: Lysine-specific porphyrinomas gingivitis
TITLE OF INVENTION: Protease
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winer, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,324
FILING DATE: 21-OCT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 44-93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-141-324-11

Query Match 100.0% Score 47: DB 1: Length 27;
Best Local Similarity 100.0% Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
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Db 2 EISEVKMDAE 11

RESULT 2

US-08-541-902-11
; Sequence 11, Application US/08541902
; Patent No. 5707620
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541.902
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/141.324
FILING DATE: 21-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Feiber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 44-93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
TELEFAX: 303-499-8089

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-541-902-11

Query Match 100.0%; Score 47; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
|1111111111|
Db 2 EISEVKMDAE 11

RESULT 3

US-08-462-859A-5
; Sequence 5, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of

;; TITLE OF INVENTION: using Same to Access Agents which Down-Regulate Formation
;; TITLE OF INVENTION: of B-Amyloid Peptide
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSEE: American Cyanamid Company
;; STREET: One Cyanamid Plaza
;; CITY: Wayne
;; STATE: New Jersey
;; COUNTRY: United States
;; ZIP: 07470-8426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462.859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3346
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-5

Query Match 100.0%; Score 47; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
|1111111111|
Db 3 EISEVKMDAE 12

RESULT 4
US-08-123-659A-5
; Sequence 5, Application US/08123659A
; Patent No. 5656477
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.

;; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
;; TITLE OF INVENTION: Using Same to Access Agents which Down-Regulate Formation
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSEE: Anne Rosenblum
;; STREET: 163 Delaware Avenue, Suite 212
;; CITY: Delmar
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 12054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123.659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.

REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-5

Query Match 100.0%; Score 47; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
|||||
DB 3 EISEVKMDAE 12

RESULT 5

US-08-464-247A-5
Sequence 5, Application US/08464247A
Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-4117
TELEFAX: 201-683-2158
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-5

Query Match 100.0%; Score 47; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
|||||
DB 3 EISEVKMDAE 12

RESULT 6
US-08-464-248A-5
Sequence 5, Application US/08464248A
Patent No. 5703209
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-5

Query Match 100.0%; Score 47; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
|||||
DB 3 EISEVKMDAE 12

RESULT 7
US-08-371-930-25
Sequence 25, Application US/08371930
Patent No. 5578451
GENERAL INFORMATION:
APPLICANT: Nishimoto, Ikuo
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,930
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/019,208
FILING DATE: February 18, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/154001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 58
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-371-930-25

Query Match 100.0%; Score 47; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
|||||
DB 40 EISEVKMDAE 49

RESULT 8
PCT-US94-01712-25
Sequence 25, Application PC/TUS9401712
GENERAL INFORMATION:
APPLICANT: Nishimoto, Ikuo
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50x or 55sx
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/019,208
FILING DATE: February 18, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/154001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 58
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US94-01712-25

Query Match 100.0%; Score 47; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
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DB 40 EISEVKMDAE 49

RESULT 9
US-08-462-859A-3
Sequence 3, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-3

Query Match 100.0%; Score 47; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EISEVKMDAE 10
|||||
DB 3 EISEVKMDAE 12

RESULT 10
US-08-462-859A-4
Sequence 4, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
NUMBER OF SEQUENCES: 19

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-4

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 63;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
DB 3 EISEVKMDAE 12

RESULT 11
US-08-123-659A-3
Sequence 3, Application US/08123659A
Patent No. 5656477
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:

```

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TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-3

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 63;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
DB 3 EISEVKMDAE 12

RESULT 12
US-08-123-659A-4
Sequence 4, Application US/08123659A
Patent No. 5656477
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-4

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 63;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EISEVKMDAE 10
DB 3 EISEVKMDAE 12

RESULT 13
US-08-464-247A-3
Sequence 3, Application US/08464247A

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; Patent No. 5693478
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,247A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,844-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-464-247A-3

Query Match      100.0%; Score 47; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EISEVKMDAE 10
Db      3 EISEVKMDAE 12

RESULT 14
US-08-464-247A-4
; Sequence 4, Application US/08464247A
; Patent No. 5693478
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/464,247A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-464-247A-4

Query Match      100.0%; Score 47; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EISEVKMDAE 10
Db      3 EISEVKMDAE 12

RESULT 15
US-08-464-248A-3
; Sequence 3, Application US/08464248A
; Patent No. 5703209
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5703209e1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,248A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-464-248A-3

Query Match      100.0%; Score 47; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0063;
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Db	3	EISEVKMDAE	12							

Search completed: October 29, 2002, 10:32:06
Job time : 9 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:21 ; Search time 23.1429 Seconds
(without alignments)
47.995 Million cell updates/sec

Title: US-09-580-018-3
Perfect score: 48
Sequence: I TSEYKMDAEP-10

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing--first-45--summaries

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22:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	48	100.0	10	22	AA62668
2	48	100.0	10	22	AA62668
3	48	100.0	11	22	AA62668
4	48	100.0	11	22	AA62668
5	48	100.0	11	22	AA62668
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8	48	100.0	11	22	AA62668
9	48	100.0	11	22	AA62668
10	48	100.0	11	22	AA62668
11	48	100.0	11	22	AA62668

12	48	100.0	23	22	AA62668	Asp2 substrate w1
13	48	100.0	33	20	AA62668	Amyloid precursor
14	48	100.0	39	21	AA62668	Beta-APP alpha-sec
15	48	100.0	45	18	AA62668	Amyloid precursor
16	48	100.0	45	18	AA62668	Amyloid precursor
17	48	100.0	45	19	AA62668	Amyloid precursor
18	48	100.0	45	19	AA62668	Deletion beta-amy1
19	48	100.0	53	16	AA62668	Variant beta amylo
20	48	100.0	54	21	AA62668	Amyloid-beta precu
21	48	100.0	57	21	AA62668	Human amyloid prec
22	48	100.0	58	15	AA62668	Amyloid precursor
23	48	100.0	63	18	AA62668	Amyloid precursor
24	48	100.0	63	18	AA62668	Amyloid precursor
25	48	100.0	63	19	AA62668	APP-REP 751 BAP pe
26	48	100.0	63	19	AA62668	APP-REP 751 BAP pe
27	48	100.0	63	19	AA62668	Beta-amyloid pepti
28	48	100.0	63	19	AA62668	Beta-amyloid pepti
29	48	100.0	67	19	AA62668	Peptide derived fr
30	48	100.0	93	22	AA62668	Novel human diagno
31	48	100.0	112	17	AA62668	Familial Alzheimer
32	48	100.0	115	20	AA62668	London-FAD APP pol
33	48	100.0	117	19	AA62668	Flag-amyloid prote
34	48	100.0	162	9	AA62668	Deduced sequence 1
35	48	100.0	162	12	AA62668	Beta-amyloid-relat
36	48	100.0	162	14	AA62668	Deduced from clone
37	48	100.0	249	15	AA62668	Beta-amyloid precu
38	48	100.0	264	10	AA62668	Protein sequence 1
39	48	100.0	264	10	AA62668	Sequence of amy 37
40	48	100.0	487	18	AA62668	Amyloid precursor
41	48	100.0	487	18	AA62668	Amyloid precursor
42	48	100.0	487	18	AA62668	APP-REP 751 protei
43	48	100.0	487	19	AA62668	Amyloid precursor
44	48	100.0	492	14	AA62668	APP-REP 751 amyloi
45	48	100.0	492	18	AA62668	Amyloid precursor

ALIGNMENTS

RESULT 1	AA62668	standard; peptide; 10 AA.
ID	AA62668	
XX	AA62668	
AC	AA62668	
XX	AA62668	
DT	17-SEP-2001 (first entry)	
XX	17-SEP-2001	
DE	Beta-sheet breaker peptide inhibitor assay related peptide #3.	
XX	Beta-sheet breaker peptide; protein conformational disease; amyloid;	
KW	Alzheimer's disease; FAF; Down' syndrome; amyloidosis disorder;	
KM	pilon disease; prion associated neurodegenerative disease.	
XX		
OS	Synthetic.	
PN	WO200134631-A2.	
XX	17-MAY-2001.	
PD	04-NOV-2000: 2000WO-US30416.	
PF	05-NOV-1999: 99US-0163911.	
PR	05-NOV-1999: 99US-0163911.	
XX		
PA	(AXON-) AXONYX INC.	
XX		
PI	Soto-Jara C.	
XX		
DR	WPI, 2001-408068/43.	
XX		
PT	New peptide analogues and mimetics, useful by oral administration for	
PT	the treatment of Alzheimer's and prion disease by stabilization of the	
PT	conformation of amyloidogenic peptide	
XX		

PS Examples; Page 28; 48pp; English.

XX The present invention relates to beta-sheet breaker peptide analogues

CC capable of inhibiting beta-pleated sheet formation in amyloid

CC beta-peptide. These are obtained by modification of a beta-sheet breaker

CC peptide. They can be used to reduce the formation of amyloid or

CC amyloid-like deposits involving abnormal folding into beta-sheet

CC structures or conformational change in prion Pr protein. They are thus

CC useful in the treatment of Alzheimer's disease, FAF, Down's syndrome,

CC other amyloidosis disorders, prion diseases such as kuru,

CC Creutzfeldt-Jakob disease, Gerstmann-Strauslert-Scheinker syndrome, prion

CC associated human neurodegenerative diseases, scrapie, spongiform

CC encephalopathy, transmissible milk encephalopathy and chronic wasting

CC disease of mule deer and elk. The present sequence is a peptide described

CC in the exemplification of the invention.

XX

SO Sequence 10 AA:

Query Match 100.0%; Score 48; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00077;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10

DB 1 ISEVKMDAEF 10

RESULT 2

AAB46207

ID AAB46207 standard; peptide: 10 AA.

XX AAB46207;

XX 04-APR-2001 (first entry)

DE Human APP derived immunogenic peptide #3.

XX

KW Amyloid deposit; APP: Abeta; brain; human; clearing response; nootropic;

KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;

KW amyloid precursor protein; Alzheimer's disease.

XX

OS Homo sapiens.

XX

PN WO200072880-A2.

XX

PD 07-DEC-2000.

XX

PF 26-MAY-2000; 2000WO-US14810.

XX

PR 28-MAY-1999; 99US-0322289.

XX

PA (NEUR-) NEURALAB LTD.

XX

PI Schenk DB, Bard F, Vasquez NJ, Yednock T;

DR WPI; 2001-032104/04.

XX

PT Preventing or treating a disease associated with amyloid deposits,

PT especially Alzheimer's disease, comprises administering amyloid

PT specific antibody -

XX

PS Disclosure; Figure 19; 143pp; English.

XX

CC This invention describes a novel method of preventing or treating a

CC disease associated with amyloid deposits of amyloid precursor protein

CC (APP) Abeta fragments in the brain of a patient, which comprises

CC administering to the patient: (a) an antibody that binds to Abeta, the

CC antibody binds to an amyloid deposit and induces a clearing response (Fc

CC receptor mediated phagocytosis) against it (b) a polypeptide containing

CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent

CC that induces an immunogenic response against residues 1-3 to 7-11 of

CC Abeta. The products of the invention have nootropic and neuroprotective

CC activity. The method is also useful for monitoring a course of treatment

CC being administered to a patient e.g. active and passive immunization. The

CC methods are useful for prophylactic and therapeutic treatment of

CC Alzheimer's disease.

XX

SO Sequence 10 AA:

Query Match 100.0%; Score 48; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00077;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10

DB 1 ISEVKMDAEF 10

RESULT 3

AAB75143

ID AAB75143 standard; peptide: 11 AA.

XX AAB75143;

XX 08-AUG-2001 (first entry)

DE APP beta-secretase cleavage site spanning peptide SEQ ID NO.1.

XX

KW Amyloid precursor protein; APP; Asp 1; endorepsin 1; inhibition;

KW transmembrane aspartyl proteinase; APP Swedish variant; nootropic;

KW neuroprotective; beta-secretase cleavage site; Alzheimer's disease;

KW beta amyloid protein-related disease; antiAlzheimer.

XX

OS Homo sapiens.

XX

PN WO200131054-A1.

XX

PD 03-MAY-2001.

XX

PF 19-OCT-2000; 2000WO-GB04028.

XX

PR 22-OCT-1999; 99GB-0025136.

XX

PA (SMK) SMITHKLINE BEECHAM PLC.

PA (SMK) SMITHKLINE BEECHAM CORP.

XX

PI Christie G, Hussain I, Powell DJ;

DR WPI; 2001-328654/34.

XX

PT Identifying inhibitors of Asp 1-mediated cleavage, for treating or

PT preventing beta-amyloid protein-related disease, comprises measuring

PT the extent of substrate cleavage in a reaction system containing Asp 1

PT and a substrate -

XX

PS Disclosure; Page 3; 31pp; English.

XX

CC The present invention describes a method of screening for compounds

CC which inhibit Asp 1-mediated cleavage of a polypeptide or protein

CC substrate. The method comprises providing a reaction system comprising

CC Asp 1 and substrate, and measuring the extent of cleavage of the

CC substrate in the presence of test compound compared with that in the

CC presence of the test compound. Also described are: (1) a method of

CC screening for compounds which inhibit Asp 1 mediated cleavage of a

CC polypeptide or protein substrate comprising providing a reaction system

CC comprising Asp 1 and a labeled active site ligand, and measuring the

CC extent of binding of the labeled ligand in the presence of test compound

CC compared with that in the presence of the test compound; (2) a compound

CC identified by the method; (3) a pharmaceutical composition comprising the

CC compound of (2) and a carrier; (4) a method of inhibiting Asp 1 modulated

CC amyloid precursor protein (APP) cleavage, or treating or prophylaxis of

CC beta-amyloid protein-related disease, comprising administering to a

CC patient a compound of (2); (5) a compound which is an inhibitor of Asp 1

CC modulated APP cleavage; and (6) a method for treating or prophylaxis of

CC beta-amyloid protein-related disease comprising administering a compound

CC of (2) or (5). The compound which inhibits Asp 1 mediated cleavage of a

CC polypeptide or protein is useful in therapy, in the preparation of a
 CC medicament for inhibiting Asp 1-modulated APP cleavage and for the
 CC treatment or prophylaxis of beta-amyloid protein-related disease,
 CC including Alzheimer's disease. The present sequence represents an APP
 CC beta-secretase cleavage site spanning peptide which can be used as a
 CC substrate in the method of the invention.

XX Sequence 11 AA:

Query Match 100.0%; Score 48; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00086;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10

DB 1 ISEVKMDAEF 10

RESULT 4

ID AAB75144 standard; peptide; 11 AA.

AC AAB75144;

DT 08-AUG-2001 (first entry)

XX Asp 1 substrate sequence SEQ ID NO:3.

DE Amyloid precursor protein; APP; Asp 1; endorepsin 1; inhibition;
 XX transmembrane aspartyl proteinase; APP Swedish variant; neurotrophic;
 KW neuroprotective; beta-secretase cleavage site; Alzheimer's disease;
 KW beta amyloid protein-related disease; antialzheimer.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 1 /note="N-terminally attached to maltose binding protein
 FT (MBP)"

XX WO200131054-A1.

XX 03-MAY-2001.

XX 19-OCT-2000; 2000WO-GB04028.

XX 22-OCT-1999; 99GB-0025136.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Christle G, Hussain I, Powell DJ;

XX WPI; 2001-328654/34.

XX Identifying inhibitors of Asp 1-mediated cleavage, for treating or
 XX preventing beta-amyloid protein-related disease, comprises measuring
 XX the extent of substrate cleavage in a reaction system containing Asp 1
 XX and a substrate -

XX Disclosure; Page 3; 31pp; English.

XX The present invention describes a method of screening for compounds
 XX which inhibit Asp 1-mediated cleavage of a polypeptide or protein
 XX substrate. The method comprises providing a reaction system comprising
 XX Asp 1 and substrate, and measuring the extent of cleavage of the
 XX substrate in the presence of test compound compared with that in the
 XX presence of the test compound. Also described are: (1) a method of
 XX screening for compounds which inhibit Asp 1 mediated cleavage of a
 XX polypeptide or protein substrate comprising providing a reaction system
 XX comprising Asp 1 and a labeled active site ligand, and measuring the
 XX extent of binding of the labeled ligand in the presence of test compound
 XX compared with that in the presence of the test compound; (2) a compound

CC identified by the method; (3) a pharmaceutical composition comprising the
 CC compound of (2) and a carrier; (4) a method of inhibiting Asp 1 modulated
 CC amyloid precursor protein (APP) cleavage, or treating or prophylaxis of
 CC beta-amyloid protein-related disease, comprising administering to a
 CC patient a compound of (2); (5) a compound which is an inhibitor of Asp 1
 CC mediated APP cleavage; and (6) a method for treating or prophylaxis of
 CC beta-amyloid protein-related disease comprising administering a compound
 CC of (2) or (5). The compound which inhibits Asp 1 mediated cleavage of a
 CC polypeptide or protein is useful in therapy, in the preparation of a
 CC medicament for inhibiting Asp 1-modulated APP cleavage and for the
 CC treatment or prophylaxis of beta-amyloid protein-related disease,
 CC including Alzheimer's disease. The present sequence represents an APP 1
 CC substrate sequence which is given in the exemplification of the present
 CC invention.

XX Sequence 11 AA:

Query Match 100.0%; Score 48; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00086;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10

DB 1 ISEVKMDAEF 10

RESULT 5

ID AAB97468 standard; Protein; 11 AA.

AC AAB97468;

DT 03-AUG-2001 (first entry)

XX Asp2 substrate wild-type beta-site peptide sequence.

XX Asp2; endorepsin 2; memapsin 2; beta-amyloid protein;

XX Alzheimer's disease; cortical Lewy body disease; Parkinson's disease;

XX Asp2 inhibitor.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /label= OTHER
 FT /note="optionally bound to maltose binding protein"

XX WO200129563-A1.

XX 26-APR-2001.

XX 19-OCT-2000; 2000WO-GB04039.

XX 21-OCT-1999; 99GB-0024957.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Christle G, Hussain I, Powell DJ;

XX WPI; 2001-300381/31.

XX Screening for inhibitors of Asp 2 mediated polypeptide cleavage
 XX comprising measuring substrate cleavage or ligand binding with a system
 XX comprising Asp 2 and a substrate or labelled ligand in the presence or
 XX absence of a test compound -

XX Disclosure; Page 3; 34pp; English.

XX The present invention describes a method of screening for compounds which
 XX inhibit Asp2 (also known as memapsin 2 and endorepsin 2) mediated
 XX cleavage of a protein substrate, involving measuring the extent of
 XX cleavage of the substrate in the presence and absence of the test

CC compound. Asp2 is thought to be involved in the cleavage of amyloid
CC precursor protein which is excised to produce beta-amyloid. Beta-amyloid
CC is involved in the pathogenesis of Alzheimer's disease, Parkinson's
CC disease, cortical Lewy body disease and vascular and cerebrovascular
CC diseases, and Asp2 inhibitors could be useful in their treatment. The
CC present sequence is an example of an Asp2 substrate.

XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 48; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00086;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
|||||
Db 1 ISEVKMDAEF 10

RESULT 6
AAW70869

ID AAW70869 standard; peptide; 13 AA.

XX AAW70869;

XX 04-FEB-1999 (first entry)

DE Beta-amyloid peptide to create a monoclonal antibody.

KW Beta-amyloid precursor protein; beta-APP; beta-amyloid peptide;
KM antibody; amyloid deposit; Alzheimer's disease.

XX Synthetic.

OS Homo sapiens.

XX MO9844955-A1.

PN 15-OCT-1998.

PD 09-APR-1998; 98WO-US06900.

PF 09-APR-1997; 97US-0041850.

PR (MCIN/) MCINNTIS P A.

PA (MIND-) MINDSET LTD.

XX Chain DG;

XX WPI; 1998-594476/50.

PT Preventing or inhibiting progression of Alzheimer's Disease -
PT comprises use of recombinant DNA encoding an antibody specific for
PT the N- or C-terminus of an amyloid-beta peptide

XX Example 1; Page 47; 58pp; English.

CC The present sequence represents a peptide derived from beta-amyloid
CC precursor protein (beta-APP). The peptide is a beta-amyloid
CC peptide and is used to produce a monoclonal antibody. The specification
CC describes a method for prevention or inhibition of progression of
CC Alzheimer's disease. The method comprises administering a composition
CC comprising a recombinant DNA molecule containing a gene encoding a
CC recombinant antibody end-specific for the N-terminus or the C-terminus
CC of an amyloid-beta peptide, operably linked to a promoter which is
CC expressed in the central nervous system. The recombinant antibody
CC molecules prevent the accumulation of beta-amyloid peptides in the
CC extracellular space, interstitial fluid and cerebrospinal fluid and the
CC aggregation of such peptides into amyloid deposits in the brain. They
CC also inhibit the progression of Alzheimer's disease by inhibiting the
CC interaction of beta-amyloid peptides mediating Alzheimer's disease
CC induced neurotoxicity and inhibiting the Alzheimer's disease induced
CC complement activation and cytokine release involved in the inflammatory
CC process.

SQ Sequence 13 AA;

Query Match 100.0%; Score 48; DB 19; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
|||||
Db 2 ISEVKMDAEF 11

RESULT 7
AAB06315

ID AAB06315 standard; peptide; 16 AA.

XX AAB06315;

DT 03-OCT-2000 (first entry)

DE Human beta-amyloid precursor protein beta-secretase cleavage site.

KW Human; beta-amyloid precursor protein; beta-APP; beta-secretase;
KM subtilisin-kexin isoenzyme 1; SKI-1;

KW pro-brain-derived neurotrophic factor; PROBDNF; antilipemic;
KM cytostatic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia;

KW liver steatosis; Ras dependent cancer; restenosis;
KM amyloid protein formation.

XX Homo sapiens.

OS Homo sapiens.

XX Key

FT Cleavage-site 8.9

PN WO200026348-A2.

PD 11-MAY-2000.

PF 04-NOV-1999; 99WO-CA01058.

PR 04-NOV-1998; 98CA-2249648.

PA (RECT-) INST RECH CLINIQUES MONTREAL.

XX Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

XX WPI; 2000-365601/31.

PT Novel soluble proteic fragment of subtilisin-kexin isoenzyme for
PT producing a polypeptide useful for treating hypercholesterolemia, liver
PT steatosis and amyloidosis, comprises a specific amino acid sequence -
PS Example 4; Page 51; 119pp; English.

XX The present sequence is the beta-secretase site of human beta-amyloid

CC precursor protein (beta-APP). The sequence may be cleaved

CC by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1

CC (SKI-1), a type-1 membrane-bound proteinase. Peptides which bind to and

CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for

CC screening inhibitors of SKI-1 activity, or for screening enhancers of

CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1

CC catalytic site may be used as inhibitors of SKI-1 activity. They may be

CC used to treat diseases involving overexpression of SKI-1 or SKI-1

CC substrate. Such diseases include hypercholesterolaemia, high levels of

CC fatty acids, lipids or larnesyl pyrophosphate, liver steatosis,

CC Ras-dependent cancer, restenosis and amyloid protein formation.

XX Sequence 16 AA;

Query Match 100.0%; Score 48; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.0013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10

DB 3 ISEVKMDAEF 12

RESULT 8

ID AAB06317 standard; peptide: 16 AA.

AC AAB06317;
XX
XX
DT 03-OCT-2000 (first entry)

DE Human beta-amyloid precursor protein beta-epsiloon1-secretase site.

XX Human; beta-amyloid precursor protein; beta-APP;
XX beta-epsiloon1-secretase; subtilisin-kexin isoenzyme 1; SKI-1;
KM pro-brain-derived neurotrophic factor; proBDNF; antilipemic;
KM cytosolic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia;
KM liver steatosis; Ras-dependent cancer; restenosis;
KM amyloid protein formation.

OS Homo sapiens.

XX
XX
XX Key Location/Qualifiers

FT Cleavage-site 8..9
XX
XX WO200026348-A2.

PD 11-MAY-2000.

XX 04-NOV-1999; 99WO-CA01058.

XX 04-NOV-1998; 98CA-2249648.

XX (RECL-) INST RECH CLINIQUES MONTREAL.

XX Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

XX WPI; 2000-365601/31.

XX Novel soluble proteic fragment of subtilisin-kexin isoenzyme for
PT producing a polypeptide useful for treating hypercholesterolemia, liver
XX steatosis and amyloidosis, comprises a specific amino acid sequence -
XX
XX Example 4; Page 51; 119pp; English.

XX The present sequence is the beta-epsiloon1-secretase site of human
CC beta-amyloid precursor protein (beta-APP). The sequence may be cleaved
CC by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1
CC (SKI-1), a type-1 membrane-bound proteinase. Peptides which bind to and
CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for
CC screening inhibitors of SKI-1 activity, or for screening enhancers of
CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1
CC catalytic site may be used as inhibitors of SKI-1 activity. They may be
CC used to treat diseases involving overexpression of SKI-1 or SKI-1
CC substrate. Such diseases include hypercholesterolaemia, high levels of
CC fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,
CC Ras-dependent cancer, restenosis and amyloid protein formation.

XX Sequence 16 AA;

Query Match 100.0%; Score 48; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
XX
XX
DB 1 ISEVKMDAEF 10

RESULT 9
AAE00608
ID AAE00608 standard; peptide: 18 AA.

XX AAE00608;

XX 02-JUL-2001 (first entry)

DE Beta-amyloid precursor protein beta-secretase cleavage site.

XX Beta-amyloid precursor protein; beta-APP; caspase; beta-secretase;
KM cysteine protease; apoptosis; caspase expression cassette; metastasis;
KM tumour; cathepsin B; urokinase; proliferation; gene therapy;
KM interdomain linker; cleavage site; Alzheimer's disease.

XX Unidentified.

XX WO200129232-A2.

PD 26-APR-2001.

XX 19-OCT-2000; 2000WO-US28941.

XX 20-OCT-1999; 99US-0160559.

XX 14-AUG-2000; 2000US-0225564.

XX (SCIO-) SCIOS INC.

XX Cordell B, Li Y;

XX WPI; 2001-290920/30.

XX Novel fusion polypeptide comprising first and second caspase subunit
PT separated by cleavage site not associated in nature with caspase
PT subunit, useful for cloning gene encoding enzymes involved in
PT proteolytic cleavage -
XX
XX Example 2; Page 26; 116pp; English.

XX The present sequence is a beta-secretase cleavage site of beta-amyloid
CC precursor protein (beta-APP). This sequence is used to construct
CC an artificially engineered chimeric cassette comprising human caspase-3
CC with interdomain linker replaced by Swedish mutant beta-secretase
CC cleavage site. This modified caspase-3 plays a pivotal role in
CC Alzheimer's disease. Caspases are a family of cysteine proteases, that
CC participate in the initiation and execution of apoptosis.
CC The present invention relates to a method for functional cloning of genes
CC encoding proteins or enzymes involved in proteolytic cleavage. The
CC invention is based on the use of caspase expression cassettes comprising
CC the coding sequence of a proteolytic cleavage site flanked by sequences
CC encoding two caspase subunits. A fusion polypeptide comprising a first
CC and a second caspase subunit, separated by a cleavage site not associated
CC in nature, is useful for cloning gene encoding enzymes involved in
CC proteolytic cleavage. An expression cassette containing fusion
CC polypeptide is used to identify a mutant cell line deficient in an
CC enzyme of interest and is also useful for diagnosis and suppression of
CC proliferation or metastases of a tumour cell characterised by
CC overexpression of a polypeptide (e.g. Cathepsin B or urokinase,
CC selectively expressed in the tumour cells). DNA encoding fusion
CC polypeptide is used in gene therapy.

XX Sequence 18 AA;

Query Match 100.0%; Score 48; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
XX
XX
DB 5 ISEVKMDAEF 14

RESULT 10
AAV69713
ID AAV69713 standard; peptide: 20 AA.

AC	AA69713:
XX	
DT	11-APR-2000 (first entry)
XX	
DE	Beta-APP alpha-secretase substrate [KM](-10,+10).
XX	
KW	Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
KM	Cleavage site; beta-secretase; neurodegenerative disease;
KW	Alzheimer's disease.
XX	
OS	Homo sapiens.
PN	M0964587-A1.
PD	16-DEC-1999.
PF	04-JUN-1999; 99MO-FR01326.
PR	05-JUN-1998; 98FR-0007068.
PR	31-MAR-1999; 99US-0122599.
XX	
PA	(RHON) RHONE-POULENC RORER SA.
PA	(UYPA-) UNIV CURIE PARIS VI P & M.
PI	Rholam M, Munoz-Gimenez N, Moutouakil M, Cohen P, Bertrand P;
DR	WPI: 2000-097537/08.
PT	Polypeptide with beta-secretase activity, specific for wild-type
XX	amyloid precursor protein, useful in treating Alzheimer's disease -
PS	Example 3; Page 24; 44pp; French.
CC	
CC	Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
CC	novel polypeptide with beta-secretase activity that can cleave
CC	specifically the natural beta-amyloid precursor protein (APP). Normal
CC	cleavage of the protein occurs between amino acids Met596-Asp597 and
CC	Val636-Ile637 (positions 4-5 and 44-45 of AA69701). The novel
CC	polypeptide is used to identify agents that interact specifically with
CC	it. These agents regulate metabolism of APP, particularly they slow down
CC	or reduce production of beta-amyloid, so can be used to treat
CC	neurodegenerative diseases, particularly Alzheimer's disease.
XX	
SQ	Sequence 20 AA;
	Query Match 100.0%; Score 48; DB 21; Length 20;
	Best Local Similarity 100.0%; Pred. No. 0.0017;
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps
OY	1 ISEVKMDAEF 10 5 ISEVKMDAEF 14
Db	
RESULT 11	
AAB75147	
ID	AAB75147 standard; peptide; 23 AA.
AC	AAB75147;
XX	
DT	08-AUG-2001 (first entry)
DE	Asp 1 substrate sequence SEQ ID NO:6.
XX	
KM	Amyloid precursor protein; APP; Asp 1; endoregulin 1; inhibition;
KM	transmembrane aspartyl protease; APP Swedish variant; nootropic;
KW	neuroprotective; beta-secretase cleavage site; Alzheimer's disease;
KM	beta amyloid protein-related disease; anti-Alzheimer.
XX	
OS	Homo sapiens.
OS	Synthetic.
Key	Location/Qualifiers
PH	

FT	Modified-site	1	/note="N-terminally attached to maltose binding protein
FT			(MBP)"
XX			
PN	WO200131054-A1.		
PD	03-MAY-2001.		
XX			
PF	19-OCT-2000; 2000WO-GB04028.		
XX			
PR	22-OCT-1999; 99GB-0025136.		
XX			
PA	(SMIK) SMITHKLINE BEECHAM PLC.		
XX	(SMIK) SMITHKLINE BEECHAM CORP.		
PI	Christie G, Hussain I, Powell DJ;		
DR	WPI; 2001-328654/34.		
PT	Identifying inhibitors of Asp 1-mediated cleavage, for treating or		
PT	preventing beta-amyloid protein-related disease, comprises measuring		
PT	the extent of substrate cleavage in a reaction system containing Asp 1		
PT	and a substrate -		
PS	Disclosure; Page 3; 31pp: English.		
XX			
CC	The present invention describes a method of screening for compounds		
CC	which inhibit Asp 1-mediated cleavage of a polypeptide or protein		
CC	substrate. The method comprises providing a reaction system comprising		
CC	Asp 1 and substrate, and measuring the extent of cleavage of the		
CC	substrate in the presence of test compound compared with that in the		
CC	presence of the test compound. Also described are: (1) a method of		
CC	screening for compounds which inhibit Asp 1 mediated cleavage of a		
CC	polypeptide or protein substrate comprising providing a reaction system		
CC	comprising Asp 1 and a labeled active site ligand, and measuring the		
CC	extent of binding of the labeled ligand in the presence of test compound		
CC	compared with that in the presence of the test compound; (2) a compound		
CC	identified by the method; (3) a pharmaceutical composition comprising the		
CC	compound of (2) and a carrier; (4) a method of inhibiting Asp 1 modulated		
CC	amyloid precursor protein (APP) cleavage, or treating or prophylaxis of		
CC	beta-amyloid protein-related disease, comprising administering to a		
CC	patient a compound of (2); (5) a compound which is an inhibitor of Asp 1		
CC	modulated APP cleavage; and (6) a method for treating or prophylaxis of		
CC	beta-amyloid protein-related disease comprising administering a compound		
CC	of (2) or (5). The compound which inhibits Asp 1 mediated cleavage of a		
CC	polypeptide or protein is useful in therapy, in the preparation of a		
CC	medicament for inhibiting Asp 1-modulated APP cleavage and for the		
CC	treatment or prophylaxis of beta-amyloid protein-related disease,		
CC	including Alzheimer's disease. The present sequence represents an Asp 1		
CC	substrate sequence which is given in the exemplification of the present		
CC	invention.		
XX			
SQ	Sequence	23 AA;	
QY	1 ISEVKMDAEP 10		
Db	1 ISEVKMDAEP 10		
RESULT 12			
AAB97473	AAB97473 standard; Protein; 23 AA.		
XX			
AC	AAB97473;		
XX			
XX	03-AUG-2001 (first entry)		
XX			
DE	Asp2 substrate wild-type beta-site C-terminal Q-tag fusion peptide.		

KM Asp2; endocrepisin 2; memapsin 2; beta-amyloid protein;
 KW Alzheimer's disease; cortical Lewy body disease; Parkinson's disease;
 XX Asp2 inhibitor.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= OTHER
 FT /note= "bound to maltose binding protein"
 XX
 PN W0200129563-A1.
 XX
 PD 26-APR-2001.
 XX
 PF 19-OCT-2000; 2000WO-GB04039.
 XX
 PR 21-OCT-1999; 99GB-0024957.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Christie G, Hussain I, Powell DJ;
 DR WPI; 2001-300381/31.
 XX
 XX Screening for inhibitors of Asp 2 mediated polypeptide cleavage
 PT comprises measuring substrate cleavage or ligand binding with a system
 PT comprising Asp 2 and a substrate or labelled ligand in the presence or
 PT absence of a test compound -
 XX
 PS Disclosure; Page 4; 34pp; English.
 XX
 CC The present invention describes a method of screening for compounds which
 CC inhibit Asp2 (also known as memapsin 2 and endocrepisin 2) mediated
 CC cleavage of a protein substrate, involving measuring the extent of
 CC cleavage of the substrate in the presence and absence of the test
 CC compound. Asp2 is thought to be involved in the cleavage of amyloid
 CC precursor protein which is excised to produce beta-amyloid. Beta-amyloid
 CC is involved in the pathogenesis of Alzheimer's disease. Parkinson's
 CC disease, cortical Lewy body disease and vascular and cerebrovascular
 CC diseases, and Asp2 inhibitors could be useful in their treatment. The
 CC present sequence is an example of an Asp2 substrate.
 CC
 XX
 SQ Sequence 23 AA;
 QY
 Query Match 100.0%; Score 48; DB 22; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 ISEVKMDAEF 10
 1 ISEVKMDAEF 10
 RESULT 13
 AAM98002
 ID AAM98002 standard; Protein; 33 AA.
 XX
 AC AAM98002;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Amyloid precursor protein (aa656-678) with Swedish mutation.
 XX
 KW Amyloid precursor protein; APP; human; gene targeting;
 KW homologous recombination; transgenic mouse; transgenic animal;
 KW animal model; Alzheimer's disease.
 XX
 OS Mus musculus.
 XX
 PN W09909150-A1.
 XX

PD 25-FEB-1999.
 XX
 PF 18-AUG-1997; 97WO-US14507.
 XX
 PR 18-AUG-1997; 97WO-US14507.
 XX
 PA (FARB) BAYER CORP.
 XX
 PI Mirak DO;
 DR WPI; 1999-181029/15.
 XX
 PT Modification of target nucleic acids - by homologous recombination,
 PT used particularly for introducing a humanised amyloid precursor
 PT protein gene into rodents for producing models of Alzheimer's
 PT disease
 XX
 PS Disclosure; Page 145; 209pp; English.
 XX
 CC This polypeptide comprises residues 656-678 of a murine amyloid
 CC precursor protein (APP). The invention provides a novel gene
 CC targeting strategy that facilitates the introduction of one or
 CC more specific mutations into any gene in a single double reciprocal
 CC homologous recombination step. The method has been used
 CC particularly for introducing a humanised APP gene into rodents for
 CC producing animal models of Alzheimer's disease (AD). 4 independent
 CC lines of transgenic mice (lines ES5007, ES5103, ES5401 and ES5403)
 CC have been created using the gene targeting technique applied to
 CC embryonic stem cells. In each line, the mouse APP gene was modified
 CC to encode a mouse/human hybrid (m/hAPP) where amino acid residues
 CC 666-770 of APP770 were encoded by human cDNA sequences instead of
 CC mouse genomic exons (exons 16-18). Within these residues, only 3
 CC amino acid differences exist between the mouse and human proteins,
 CC i.e. Gly-676 to Arg, Phe-681 to Thr and Arg-684 to His. The
 CC exon-cDNA fusion gene therefore encodes an APP containing a
 CC humanised beta-amyloid domain. Swedish- and/or London-FAD APP
 CC mutations have also been introduced (see also AAM97997-W98001).
 CC
 XX
 SQ Sequence 33 AA;
 QY
 Query Match 100.0%; Score 48; DB 20; Length 33;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 ISEVKMDAEF 10
 1 ISEVKMDAEF 10
 RESULT 14
 AAY69717
 ID AAY69717 standard; peptide; 39 AA.
 XX
 AC AAY69717;
 XX
 DT 11-APR-2000 (first entry)
 XX
 DE Beta-APP alpha-secretase substrate [KM]-APP(-20,+20).
 XX
 KW Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
 KW cleavage site; beta-secretase; neurodegenerative disease;
 KW Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN W09964587-A1.
 XX
 PD 16-DEC-1999.
 XX
 PF 04-JUN-1999; 99WO-FR01326.
 XX
 PR 05-JUN-1998; 98FR-0007068.
 PR 31-MAR-1999; 99US-0122599.

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XX (RHON ) RHONE-POULENC ROREZ SA.
PA (UYRA-) UNIV CURIE PARIS VI P & M.
XX
XX Rhojam M, Munoz-Glamez N, Moutaouakil M, Cohen P, Bertrand P;
PI WPI; 2000-097537/08.
XX
XX Polypeptide with beta-secretase activity, specific for wild-type
PT amyloid precursor protein, useful in treating Alzheimer's disease -
XX
XX Example 3; Page 24; 44pp; French.
XX
XX Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
CC novel polypeptide with beta-secretase activity that can cleave
CC specifically the natural beta-amyloid precursor protein (BAP). Normal
CC cleavage of the protein occurs between amino acids Met596-Asp597 and
CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
CC polypeptide is used to identify agents that interact specifically with
CC it. These agents regulate metabolism of APP, particularly they slow down
CC or reduce production of beta-amyloid, so can be used to treat
CC neurodegenerative diseases, particularly Alzheimer's disease.
XX
SQ Sequence 39 AA;
Query Match 100.0%; Score 48; DB 21; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ISEVKMDAEF 10
Db 14 ISEVKMDAEF 23

```

RESULT 15

AAW26512
ID AAW26512 standard; Peptide: 45 AA.
XX
AC AAW26512;
XX
DF 06-JAN-1998 (first entry)
XX
DE Amyloid precursor protein fragment APP-REP 751 (BAP del11-28).
XX
XX Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KW substrate; muten; secretase; Alzheimer's disease; human.
XX
OS Chimeric Homo sapiens.
OS Chimeric synthetic.
XX
XX
XX Key Location/Qualifiers
FH Cleavage-site 7..8
FT /note= "secretase cleavage site"
FT Peptide 10..33
FT /label= BAP(del11-28)
FT /note= "truncated beta-amyloid protein"
FT Domain 20..42
FT /label= Transmembrane
XX
XX US5656477-A.
XX
XX 12-AUG-1997.
XX
XX 01-MAY-1992: 92US-0877675.
XX
XX 20-SEP-1993: 93US-0123659.
XX
XX 01-MAY-1992: 92US-0877675.
XX
XX (AMCY) AMERICAN CYANAMID CO.
XX
XX Jacobsen JS, Vittek MP;
XX WPI; 1997-414594/38.
XX

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XX Nucleic acid encoding amyloid precursor muten(s) - comprising
PT reporter gene and coding sequence, for identifying compounds which
PT modify the activity of proteolytic enzymes which cleave APP
XX
XX Disclosure; Fig 5A: 84pp; English.
XX
XX This peptide sequence shows the region of amyloid precursor protein
CC (APP) that includes a truncated beta-amyloid protein (BAP) lacking
CC the native secretase cleavage/recognition site. In an attempt to
CC engineer an APP non-cleavable substrate for secretase, an
CC APP-reporter (APP-REP) protein that carries the BAP deletion has
CC been expressed in recombinant host cells. Deletion of these 18
CC amino acids, however, still resulted in the secretion of an
CC N-terminal APP-reporter fragment into the cytoplasm. Non-
CC cleavable APP substrates can be used to detect other putative
CC abnormal APP processing events. They can also be used to
CC investigate cellular post-translational modifications to APP in
CC order to determine the potential influence on normal secretase and
CC abnormal BAP 'clipping' activities.
XX
SQ Sequence 45 AA;
Query Match 100.0%; Score 48; DB 18; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ISEVKMDAEF 10
Db 4 ISEVKMDAEF 13

```

Search completed: October 29, 2002, 10:26:43
Job time : 24.1429 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:36 ; Search time 10.4286 Seconds
(without alignments)
92.140 Million cell updates/sec

Title: US-09-580-018-3
Perfect score: 48
Sequence: 1 ISEVKMDAEF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR-71:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	82	P00438	Alzheimer's disease
2	48	100.0	695	A49795	Alzheimer's disease
3	48	100.0	695	A27485	Alzheimer's disease
4	48	100.0	695	S00550	Alzheimer's disease
5	48	100.0	770	ORH04	Alzheimer's disease
6	44	91.7	33	S23094	beta-amyloid prote
7	44	91.7	57	E60045	Alzheimer's disease
8	44	91.7	57	F60045	Alzheimer's disease
9	44	91.7	57	G60045	Alzheimer's disease
10	44	91.7	57	D60045	Alzheimer's disease
11	44	91.7	57	A60045	Alzheimer's disease
12	44	91.7	57	B60045	Alzheimer's disease
13	42	87.5	747	JH0773	Alzheimer's disease
14	34	70.8	142	E89026	hypothetical prote
15	34	70.8	400	E69446	conserved hypotet
16	34	70.8	626	AF0358	transcription anti
17	34	70.8	700	E84131	chondroitin sulfat
18	34	70.8	3562	A47171	hypothetical prote
19	33	68.8	242	C96606	MNDH dehydrogenase
20	33	68.8	389	G84245	accessory coloniza
21	33	68.8	626	E82273	conserved hypotet
22	32	66.7	261	C64572	hypothetical prote
23	32	66.7	281	F71867	taurine transport
24	32	66.7	282	AH3629	hypothetical prote
25	32	66.7	282	T31922	hypothetical prote
26	32	66.7	347	T31922	PMO-protein - Chlo
27	32	66.7	354	S51143	44.7K vira protein
28	32	66.7	400	S70187	probable trehalase
29	32	66.7	426	G75187	

30	32	66.7	470	2	C75591	threonine synthase
31	32	66.7	793	2	T27133	hypothetical prote
32	32	66.7	929	2	T52517	hypothetical prote
33	32	66.7	941	2	B96553	hypothetical prote
34	32	66.7	1378	2	G88637	protein F53H1.4 il
35	32	66.7	1456	1	WMGCPV	RNA-directed RNA p
36	32	66.7	1906	2	AD2443	hypothetical prote
37	32	66.7	4563	1	LPMB	apolipoprotein B-1
38	32	66.7	84	2	T27174	hypothetical prote
39	31	64.6	105	2	PH1526	gamma-aminobutyric
40	31	64.6	178	2	G64168	hypothetical prote
41	31	64.6	182	2	AC0449	conserved hypotet
42	31	64.6	182	2	B97000	hypothetical prote
43	31	64.6	183	2	S56460	probable alpha hel
44	31	64.6	183	2	C91280	probable alpha hel
45	31	64.6	183	2	C86121	probable alpha hel

ALIGNMENTS

RESULT 1

P00438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995

C:Accession: P00438; C60045

R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs

A:Reference number: P00438; MUID:93075180

A:Accession: P00438

A:Molecule type: DNA

A:Residues: 1-82 <NAV>

A:Cross-references: GB:M83558; GB:M83657

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MUID:92017079

A:Accession: C60045

A:Molecule type: mRNA

A:Residues: 12-68 <JOB>

A:Cross-references: EMBL:X56129

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match

Best local similarity 100.0%; Score 48; DB 2; Length 82;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

11 ISEVKMDAEF 20

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

1 ISEVKMDAEF 10

Query Match 100.0%; Score 48; DB 1; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.048;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10
 |||||||||
 Db 591 ISEVKMDAEF 600

RESULT 3

A27485

Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse

N:Alternate names: proteinase nexin II

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text change 13-Aug-1999

C:Accession: A27485; S19727; I49485

R:Yamada, T.; Sasaki, H.; Futuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.

Biochem. Biophys. Res. Commun. 149, 665-671, 1987

A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor

A:Reference number: A27485; MUID:88106489

A:Accession: A27485

A:Molecule type: mRNA

A:Residues: 1-695 <XAM>

A:Cross-references: GB:M18373; NID:9191568; PIDN:AAA37139.1; PID:9309085

A:Experimental source: brain

R:de Strooper, B.; van Leeuwen, F.; van den Berghe, H.

Biochim. Biophys. Acta 1129, 141-143, 1991

A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer

A:Reference number: S19727; MUID:92096458

A:Accession: S19727

A:Molecule type: mRNA

A:Residues: 1-210, G, 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>

A:Cross-references: EMBL:X59379

R:Izumai, R.; Yamada, T.; Yoshikaki, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.

Gene 112, 189-195, 1992

A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's

A:Reference number: I49485; MUID:92209998

A:Accession: I49485

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-19 <RRS>

A:Cross-references: GB:J010603; NID:9220328; PIDN:BA01456.1; PID:9220329

C:Genetics:

A:Map position: 16C3

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase I

C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match

Best Local Similarity 100.0%; Score 48; DB 2; Length 695;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10

|||||||

Db 591 ISEVKMDAEF 600

Alzheimer's disease amyloid beta protein precursor - rat

N:Alternate names: beta-A4 amyloid protein

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text change 13-Aug-1999

C:Accession: S00550; A1245; A39820; S46231

R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.

A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan co

A:Reference number: A41245; MUID:88264430

A:Accession: A41245

A:Molecule type: protein

A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>

A:Note: evidence for heparan sulfate attachment

R:Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.

FEBS Lett. 349, 109-116, 1994

A:Title: The beta-A4 amyloid precursor protein binding to copper.

A:Reference number: S46251; MUID:94320627

A:Contents: annotation; copper binding sites

A:Note: rat peptides were isolated but not sequenced

R:Tompecka, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.

J. Biol. Chem. 266, 8464-8469, 1991

A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat b

A:Reference number: A39820; MUID:91217087

A:Accession: A39820

A>Status: preliminary

A:Molecule type: protein

A:Residues: 18-32 <POT>

A:Experimental source: brain

C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein

F:625-648/Domain: transmembrane #status predicted <TM>

Query Match

Best Local Similarity 100.0%; Score 48; DB 2; Length 695;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10

|||||||

Db 591 ISEVKMDAEF 600

RESULT 5

ORH04

Alzheimer's disease amyloid beta protein precursor [validated] - human

N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inh

N:Contains: amyloid beta protein long; plaque form; amyloid beta protein short; vascu

protein precursor splice form APP(770)

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence revision 28-Jul-1995 #text change 15-Sep-2000

C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39453; I59562;

4668; A28583; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S38252;

R:Lemire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayley, R.M.; Unterbeck, A.;

Nucleic Acids Res. 17, 517-522, 1989

A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encode

A:Reference number: S02260; MUID:89128427

A:Accession: S02260

A:Molecule type: DNA

A:Residues: 1-288, 'V', 365-770 <LEM1>

A:Cross-references: EMBL:X13466

A:Note: alternative splice form APP(695)

R:Lemire, H.G.

submitted to the EMBL Data Library, November 1988

A:Reference number: S05194

A:Accession: S05194

A:Molecule type: DNA

A:Residues: 1-14, 'V', 17-288, 'V', 365-770 <LEM2>

A:Reference number: A33260; MUID:89392030
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 656-737 <TOH>
 A:Cross-references: GB:M29270; NID:q178663; PIDN:AAA51768.1; PID:q178665
 R:Prelli, F.; Levy, E.; van Duren, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
 Blochm. Biophys. Res. Commun. 170, 301-307, 1990
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
 A:Reference number: A35486; MUID:90321244
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRE1>
 A:Note: 693-Gln was found in DNA isolated from HCHMA-D patients
 R:Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 87, 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A:Reference number: 139451; MUID:90236318
 A:Accession: 139451
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMH
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: GB:M3112; NID:q178613; PIDN:AA59502.1; PID:q178616
 A:Accession: 139451
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMH
 A:Molecule type: DNA
 A:Residues: 1-530, 'QMMPVTPAFWEAKVGR' <YOS2>
 A:Cross-references: GB:M34875; NID:q178608; PIDN:AA59501.1; PID:q178615
 R:Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168
 A:Accession: A59020
 A:Contents: annotation; extratum
 A:Note: revised physical map for reference 139451
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
 Science 248, 1124-1126, 1990
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
 A:Reference number: 139453; MUID:90260663
 A:Accession: 139453
 A:Molecule type: DNA
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: GB:M37896; NID:q178618; PIDN:AAA51727.1; PID:q178620
 A:Note: a mutation with 693-Gln is presented
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheim
 A:Reference number: 159562; MUID:92022553
 A:Accession: 159562
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716, 'F', 718-737 <MUR>
 A:Cross-references: GB:S57665; NID:q236720; PIDN:AA19991.1; PID:q236721
 R:Ramano, K.; Orr, H.T.; Payami, H.; Wjisman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukulski, W.; Larson, E.; Heston, L.L.; Martin,
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
 A:Reference number: AA4017; MUID:93035397
 A:Accession: AA4017
 A:Molecule type: DNA
 A:Residues: 687-692, 'G', 694-718 <KAM1>
 A:Cross-references: GB:S45136; NID:q257379; PIDN:AA23646.1; PID:q257380
 A:Experimental source: familial Alzheimer disease family 11T
 A:Note: sequence extracted from NCBI backbone (NCBIF:115376)
 R:Kang, J.; Lemire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grieschik, K.H.;
 Nature 325, 733-736, 1987
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac
 A:Reference number: A05134; MUID:87144572

A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288, 'V', 365-770 <KAN>
 A:Cross-references: GB:X00264; NID:q28525; PIDN:CAA68374.1; PID:q28526
 A:Note: alternative splice form APP(695)
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascula
 A:Reference number: A29030; MUID:87231971
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A:Cross-references: GB:M16765; NID:q178539; PIDN:AAA51722.1; PID:q178540
 A:Note: the authors translated the codon CAG for residue 647 as Asp
 R:Goldhaber, D.; Lemman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A:Title: Characterization and chromosomal localization of a cDNA encoding brain amylo
 A:Reference number: A47584; MUID:87120328
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756, 'S', 758-770 <GOL>
 A:Cross-references: GB:M15533; NID:q178706; PIDN:AAA5540.1; PID:q178707
 A:Experimental source: Draln
 R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van
 Science 235, 880-884, 1987
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near
 A:Reference number: A47585; MUID:87120329
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TANI>
 A:Cross-references: GB:M15532; NID:q177957; PIDN:AAA51564.1; PID:q177958
 R:Dyck, T.; Weldmann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mue
 EMBO J. 7, 949-957, 1988
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 p
 A:Reference number: S02638; MUID:8826437
 A:Accession: S02638
 A:Molecule type: mRNA
 A:Residues: 672-678 <DYR>
 R:Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; N
 Nature 331, 528-530, 1988
 A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc
 A:Reference number: S00707; MUID:88122640
 A:Accession: S00707
 A:Molecule type: mRNA
 A:Residues: 286-344, 'I', 365-366 <TAN2>
 A:Cross-references: EMBL:X06982; NID:q28817; PIDN:CAA30042.1; PID:q28812
 A:Experimental source: EMBL: X06982; NID:q28817; PIDN:CAA30042.1; PID:q28812
 A:Note: alternative splice form APP(751)
 R:Ponte, P.; Gonzalez-Demhilt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.;
 Nature 331, 525-527, 1988
 A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhi
 A:Reference number: S00925; MUID:88122639
 A:Accession: S00925
 A:Molecule type: mRNA
 A:Residues: 1-344, 'I', 365-770 <PO2>
 A:Cross-references: GB:X06989; EMBL:X00297; NID:q28720; PIDN:CAA30050.1; PID:q28721
 A:Note: alternative splice form APP(751)
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi
 A:Reference number: A38949; MUID:88122641
 A:Accession: A38949
 A:Molecule type: mRNA
 A:Residues: 287-367 <KIT>
 A:Cross-references: GB:X06981; NID:q28816; PIDN:CAA30041.1; PID:q28811
 A:Experimental source: fibroblastoma cell line
 A:Note: alternative splice form APP(770)
 R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre
 A:Reference number: A30320
 A:Accession: A30320
 A:Status: not compared with conceptual translation

A:Molecule type: mRNA
A:Residues: 284-288,'V',365-770 <VIT1>
A:Accession: B30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288,'V',365-770 <VIT2>
A:Accession: C30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 929-933, 1988
A:Title: Molecular cloning of amyloid CDNA derived from mRNA of the Alzheimer disease br
A:Reference number: A31087; MUID:88124954
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAI>
A:Cross-references: GB:M18734; NID:q178572; PID:AA51726.1; PID:q178573
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603
8 as Val, GGC for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 65
A:Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Masters, C.L.; Muthaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K.

Query Match 100.0%; Score 48; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEF 10
|||||||
DB 666 ISEVKMDAEF 675

RESULT 6
S23094

beta-amyloid protein precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C:Accession: S23094
R:Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
A:Reference number: S23094; MUID:92316198
A:Accession: S23094
A:Molecule type: protein
A:Residues: 1-33 <KOJ>
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 91.7%; Score 44; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SEVKMDAEF 10
|||||||
DB 1 SEVKMDAEF 9

RESULT 7
E60045

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C:Species: Ovis sp. (sheep)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: E60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56130
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.7%; Score 44; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SEVKMDAEF 10
|||||||
DB 1 SEVKMDAEF 9

RESULT 8
F60045

Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: F60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56127; NID:q1895; PID:CAA39592.1; PID:q1896
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.7%; Score 44; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SEVKMDAEF 10
|||||||
DB 1 SEVKMDAEF 9

RESULT 9
G60045

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.7%; Score 44; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SEVKMDAEF 10
|||||||
DB 1 SEVKMDAEF 9

RESULT 10
D60045

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: D60045
A:Molecule type: mRNA

A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56124
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.7%; Score 44; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 SEVKMDAEF 10
 |||||
 Db 1 SEVKMDAEF 9

RESULT 11
 A60045
 Alzheimer's disease amyloid beta/M protein precursor - dog (fragment)

C:Species: Canis lupus familiaris (dog)
 C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C:Accession: A60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog;
 A:Reference number: A60045; MUID:92017079

A:Accession: A60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56125

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.7%; Score 44; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 SEVKMDAEF 10
 |||||
 Db 1 SEVKMDAEF 9

RESULT 12
 B60045
 Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)

C:Species: Ursus maritimus (polar bear)
 C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
 C:Accession: B60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog;
 A:Reference number: A60045; MUID:92017079

A:Accession: B60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56128; NID:92165; PIDN:CAA3593.1; PID:92166

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.7%; Score 44; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 SEVKMDAEF 10
 |||||
 Db 1 SEVKMDAEF 9

RESULT 13
 JH0773

Alzheimer's disease amyloid beta protein precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999

C:Accession: JH0773
 R:Okado, H.; Okamoto, H.

Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992

A:Title: A Xenopus homolog of the human beta-amyloid precursor protein: development

A:Reference number: JH0773; MUID:93129227

A:Accession: JH0773

A:Molecule type: mRNA

A:Residues: 1-747 <OKA>

A:Cross-references: GB:S52417; NID:9263150; PIDN:AAB24853.1; PID:9263151

A:Experimental source: larva

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; amyloid

F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 87.5%; Score 42; DB 2; Length 747;
 Best Local Similarity 80.0%; Pred. No. 1;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ISEVKMDAEF 10
 |||||
 Db 643 ISEVKMDSEY 652

RESULT 14
 E89026

protein F13A2.1 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

C:Accession: E89026

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio

A:Reference number: A75000; MUID:99066613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;

A:Accession: E89026

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-142 <STO>

A:Cross-references: GB:chr_V; PIDN:AAB69895.1; PID:92384795; GSPDB:GN00023; CESP:F13A

C:Genetics:

A:Gene: F13A2.1

A:Map position: 5

Query Match 70.8%; Score 34; DB 2; Length 142;
 Best Local Similarity 75.0%; Pred. No. 8.1;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 3 EYVKMDAEF 10
 |||||
 Db 56 EIKQDAEF 63

RESULT 15
 E69446
 hypothetical protein AF1574 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Nov-1999

C:Accession: E69446

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Skyes,

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch

A:Reference number: A69250; MUID:98049343

A:Accession: E69446

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-400 <KIB>

A:Cross-references: GB:AF000994; GB:AF000782; NID:92689317; PIDN:AAB89681.1; PID:9264

C:Superfamily: Archaeoglobus fulgidus hypothetical protein AF1574

Query Match 70.8%; Score 34; DB 2; Length 400;

Tue Oct 29 11:23:30 2002

us-09-580-018-3.rpr

Page 6

Best Local Similarity 70.0%; Pred. No. 25;
Matches 7; Conservative 2; Mismatches

1; Indels

0; Gaps 0;

QY 1 ISEVKMDAEF 10
|:|:|:|
Db 143 ITEVKVKAEF 152

Search completed: October 29, 2002, 10:31:00
Job time : 12.4286 secs

GenCore version 5.1.3
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OK protein - protein search, using sw model

Run on: October 29, 2002, 10:22:36 ; Search time 5 Seconds

(without alignments)
77.439 Million cell updates/sec

Title: US-09-580-018-3

Perfect score: 48

Sequence: 1 ISEVKMADEF 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	48	100.0	58 1 A4_CANFA	Q28380 canis faml
2	48	100.0	59 1 A4_BOVIN	Q28053 bos taurus
3	48	100.0	751 1 A4_SAISC	Q95241 salmili scl
4	48	100.0	770 1 A4_HUMAN	P05067 homo sapien
5	48	100.0	770 1 A4_MOUSE	P12023 mus musculi
6	48	100.0	770 1 A4_RAT	P08592 rattus norv
7	44	91.7	57 1 A4_PIG	Q29023 sus scrofa
8	44	91.7	57 1 A4_URSUMA	Q29149 ursus marit
9	44	91.7	58 1 A4_RABIT	Q28748 oryctolagus
10	44	91.7	58 1 A4_SHEEP	Q28757 ovis aries
11	34	70.8	400 1 YF74_ARCFU	Q28698 archaeoglob
12	34	70.8	3562 1 PGCV_CHICK	Q90953 gallus gall
13	32	66.7	269 1 T2S1_STREPT	Q52512 streptomyce
14	32	66.7	354 1 BCPIA_CHILT	Q46135 chlorobium
15	32	66.7	365 1 BCPIA_CHILT	Q46135 chlorobium
16	32	66.7	1456 1 RRPO_PVX	P09395 potato vitu
17	32	66.7	1456 1 RRPO_PVX3	P17779 potato vitu
18	32	66.7	4563 1 APB_HUMAN	P04114 homo sapien
19	31	64.6	178 1 YJGA_HAINT	P45076 haemophilus
20	31	64.6	183 1 YJGA_ECOLI	P26506 escherichia
21	31	64.6	363 1 R1BB_PHOPO	P51562 photobacter
22	31	64.6	419 1 P47K_PSECL	P51521 pseudomonas
23	31	64.6	1017 1 MCM6_YEAST	P53091 saccharomyc
24	31	64.6	1024 1 Y075_MYCGE	P47321 mycoplasma
25	30	62.5	112 1 RBPA_MYCGE	P47389 mycoplasma
26	30	62.5	127 1 ILBP_PIG	P10289 sus scrofa
27	30	62.5	187 1 TRE1_SALTI	P12057 salmoneila
28	30	62.5	261 1 YN10_ARCFU	Q27974 archaeoglob
29	30	62.5	265 1 YGL7_YEAST	P53133 saccharomyc
30	30	62.5	304 1 PH85_KLILA	Q92241 kluyveromyc
31	30	62.5	305 1 PH85_YEAST	P17157 saccharomyc
32	30	62.5	463 1 YD14_SCHPO	Q92342 schizosacch
33	30	62.5	464 1 SPN5_SCHPO	P48010 schizosacch

34	30	62.5	656 1 V091_FOWPV	Q72896 fowlpox vir
35	30	62.5	855 1 HAUS_YEAST	P38970 saccharomyc
36	30	62.5	863 1 PHSG_MYCTU	Q10639 mycobacteri
37	30	62.5	1514 1 NX1A_RAT	Q63372 rattus norv
38	30	62.5	4639 1 DYHC_DROME	P37272 drosophila
39	29	60.4	78 1 RLF1_RICPR	Q9247 rickettsia
40	29	60.4	185 1 RRF_ECOLI	P16174 escherichia
41	29	60.4	214 1 SC14_SCHCO	P35795 schizophyll
42	29	60.4	227 1 G786_HUMAN	Q92520 homo sapien
43	29	60.4	274 1 YA99_SCHPO	Q09787 schizosacch
44	29	60.4	279 1 RPA2_SCHPO	Q92373 schizosacch
45	29	60.4	326 1 CC14_CAEEL	P18834 caenorhabdi

ALIGNMENTS

```

RESULT 1
A4_CANFA STANDARD: PRT: 58 AA.
ID A4_CANFA
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: X56125; CAA39590.1; -.
DR HSSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 49
FT CHAIN 7 49
FT DOMAIN <1 34
FT TRANSMEM 35 58
FT NON_TER 58 58
SQ SEQUENCE 58 AA: 6285 MW; 8469D488A2E12DFA CRC64;
Query Match 100.0%; Score 48; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ISEVKMADEF 10
|||||

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Db      1 ISEVKMDAEF 10

RESULT 2
A4_BOVIN STANDARD; PRT; 59 AA.
ID A4_BOVIN
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (fragment).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OC NCBI_TaxID=9913;
OX
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; Pubmed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC -----
DR EMBL: X56124; CAA39589.1; -
DR EMBL: X56126; CAA39591.1; -
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neuropeptide; Transmembrane.
FT CHAIN 1 49
FT DOMAIN <1 34 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRASMEM 35 58 POTENTIAL.
FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
FT NON_TER 59 59
SO SEQUENCE 59 AA; 6414 MW; F43469D48A2E12D CRC64;

Query Match 100.0%; Score 48; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10
DB 1 ISEVKMDAEF 10

RESULT 3
A4_SAISC STANDARD; PRT; 751 AA.
ID A4_SAISC
AC Q95241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-
```

```
DE amyloid protein (Beta-APP) (A-beta)].
GN APP.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OC NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96108492; Pubmed=8532114;
RA Levy E., Amorim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with
RT cerebral amyloid angiopathy."
RL Neurobiol. Aging 16:805-808(1995).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: S81024; AAD14347.1; -
DR HSSP: P05067; 1AAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOID4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neuropeptide; Transmembrane; Alternative splicing;
KW Signal; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 751
FT CHAIN 653 695
FT DOMAIN 18 680
FT DOMAIN 681 704
FT TRANSMEM 705 751
FT DOMAIN 287 345
FT SITE 740 743
FT ACT_SITE 301 302
FT DISULFID 291 341
FT DISULFID 300 324
FT DISULFID 316 337
FT CARBOHYD 523 523
FT CARBOHYD 552 552
SO SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 751;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10
DB 647 ISEVKMDAEF 656
```


RESULT 4
 A4_HUMAN STANDARD: PRT: 770 AA.
 AC P05067; P09000; Q16011;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II)
 DE (PN-II) (APP) [containing: Beta-amyloid protein (Beta APP) (A-beta)].
 GN APP OR A4 OR CVAP OR ADL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=87144572; PubMed=2881207;
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
 RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
 cell-surface receptor.";
 RL Nature 325:733-736(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8812639; PubMed=2893289;
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
 RA Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine
 proteinase inhibitors.";
 RL Nature 331:525-527(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89128427; PubMed=2783775;
 RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The Peda(69) precursor protein of Alzheimer's disease A4 amyloid
 is encoded by 16 exons.";
 RL Nucleic Acids Res. 17:517-522(1989).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97263807; PubMed=9108164;
 RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [5]
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
 RX MEDLINE=8812640; PubMed=2893290;
 RA Tanzi R.E., McClatchey A.I., Lampertl E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 RN [6]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=8812641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity.";
 RL Nature 331:530-532(1988).
 RN [7]
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
 RX MEDLINE=87231971; PubMed=3035574;
 RA Rokakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [8]

RP SEQUENCE OF 507-770 FROM N.A.
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [9]
 RP SEQUENCE OF 672-681.
 RX MEDLINE=88035004; PubMed=3312495;
 RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tourtellotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels.";
 RL J. Neurochem. 49:1394-1401(1987).
 RN [10]
 RP SEQUENCE OF 739-770 FROM N.A.
 RX MEDLINE=90236318; PubMed=2110105;
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";
 RL Gene 87:257-263(1990).
 RN [11]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [12]
 RP SEQUENCE OF 18-50.
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [13]
 RP IDENTITY OF APP WITH NEXIN-II.
 RX MEDLINE=89384866; PubMed=2506449;
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
 RA Sinha S.;
 RT "The secreted form of the Alzheimer's amyloid precursor protein with
 RT the Kunitz domain is protease nexin-II.";
 RL Nature 341:144-147(1989).
 RN [14]
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RX MEDLINE=90211252; PubMed=1969731;
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
 RT disease amyloid protein precursor.";
 RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
 RN [15]
 RP COMPLEX WITH G(O).
 RX MEDLINE=93188965; PubMed=8446172;
 RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
 RA Murayama Y., Ogata E.;
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 RT protein G(O).";
 RL Nature 362:75-79(1993).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
 RX MEDLINE=99215582; PubMed=10201399;
 RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinstry W.J.,
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RT "Crystal structure of the N-terminal, growth factor-like domain of
 RT Alzheimer amyloid precursor protein.";
 RL Nat. Struct. Biol. 6:327-331(1999).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.

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RX MEDLINE-91104913; PubMed-2125487;
RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kosiakof A.A.;
RT "X-ray crystal structure of the protease inhibitor domain of
RT Alzheimer's amyloid beta-protein precursor."
RL Biochemistry 29:10018-10022(1990).
[18]
RP STRUCTURE BY NMR OF 289-344.
RX MEDLINE-92031486; PubMed-1718421;
RA Heald S.L., Tilton R.F., Jr., Hammond L.S., Lee A., Bayney R.M.,
RA Kanarck M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterdeck A.,
RA Tamburini P.P.;
RT "Sequential NMR resonance assignment and structure determination of
RT the knitz-type inhibitor domain of the Alzheimer's beta-amyloid
RT precursor protein."
RL Biochemistry 30:10467-10478(1991).
[19]
RP STRUCTURE BY NMR OF 672-699.
RX MEDLINE-94281210; PubMed-7516706;
RA Talafoos J., Marchowski K.J., Klopman G., Zagorski M.G.;
RT "Solution structure of residues 1-28 of the amyloid beta-peptide."
RL Biochemistry 33:7786-7796(1994).
[20]
RP STRUCTURE BY NMR OF 696-706.
RX MEDLINE-97128622; PubMed-8973180;
RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
RT membrane-mimicking environment."
RL Biochemistry 35:16094-16104(1996).
[21]
RP STRUCTURE BY NMR OF 672-711.
RX MEDLINE-98359783; PubMed-9693002;
RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle
RT environment. Is the membrane-spanning domain where we think it is?"
RL Biochemistry 37:11064-11077(1998).
[22]
RP STRUCTURE BY NMR OF 672-689.
RX MEDLINE-20400066; PubMed-10940222;
RA Poulsen S.-A., Watson A.A., Craik D.J.;
RT "Solution structures in aqueous SDS micelles of two amyloid beta
RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
RT site."
RL J. Struct. Biol. 130:142-152(2000).
[23]
RP STRUCTURE BY NMR OF 681-706.
RX MEDLINE-20400065; PubMed-10940221;
RA Zhang S., Iwata K., Lachemann M.J., Peng J.W., Li S., Stinson E.R.,
RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;
RT "The Alzheimer's peptide A beta adopts a collapsed coil structure in
RT water."
RL J. Struct. Biol. 130:130-141(2000).
[24]
RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
RX MEDLINE-88296437; PubMed-2900137;
RA Dykys T., Wiedemann A., Muthaup G., Salbaum J.M., Lemaire H.-G.,
RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
RT "Identification, transmembrane orientation and biogenesis of the
RT amyloid A4 precursor of Alzheimer's disease."

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Query Match 100.0%; Score 48; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ISEVKMDAEF 10
DB 666 ISEVKMDAEF 675

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RESULT 5
ID A4_MOUSE STANDARD; PRT: 770 AA.
AC P12023;
DT 01-OCT-1989 (Rel. 12, Created)

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DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (Ag).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC STRAIN=BAIB/C; TISSUE=Brain;
RX MEDLINE-92096458; PubMed-1756177;
RA de Strooper B., van Leuven F., van den Bergh H.;
RT "The amyloid beta protein precursor or protease nexin II from mouse
RT is closer related to its human homolog than previously reported."
RL Biochim. Biophys. Acta 1129:141-143(1991).
[2]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE-88106489; PubMed-3322280;
RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT "Complementary DNA for the mouse homolog of the human amyloid beta
RT protein precursor."
RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
[3]
RP REVISIONS.
RA Yamada T.;
RL Submitted (MAR-1988) to the EMBL/Genbank/DBJ databases.
[4]
RP SEQUENCE OF 289-364 FROM N.A.
RC STRAIN=CD-1; TISSUE=Placenta;
RX MEDLINE-89345111; PubMed-2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RT precursor of Mus domestics."
RL Nucleic Acids Res. 17:5396-5396(1989).
[5]
RP SEQUENCE OF 1-19 FROM N.A.
RX MEDLINE-92209998; PubMed-1555768;
RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA Sakai Y.;
RT "Positive and negative regulatory elements for the expression of the
RT Alzheimer's disease amyloid precursor-encoding gene in mouse."
RL Gene 112:189-195(1992).
[6]
RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain and Kidney;
RX MEDLINE-89149813; PubMed-2493250;
RA Yamada T., Sasaki H., Donura K., Goto I., Sakaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RT for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor."
RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
[7]
RP SUBCELLULAR LOCATION: Type I membrane protein.
[8]
RP SUBCELLULAR PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
RP APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
RP SPLICING.
[9]
RP TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
RP WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
RP LIVER.
[10]
RP DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
RP WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
RP RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
RP NEXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
RP PHOSPHORYLATION (BY SIMILARITY).
[11]
RP STIMULATORY: BELONGS TO THE APP FAMILY.
[12]
RP SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
[13]
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DR EMBL: X59379; NOT_ANNOTATED_CDS.
 DR EMBL: M18373; AAA37139.1; -;
 DR EMBL: X15210; CAA33280.1; -;
 DR EMBL: D10603; BAA01456.1; -;
 DR EMBL: M24397; AAA39929.1; -;
 DR PIR: A27485; A27485.
 DR PIR: S04855; S04855.
 DR PIR: S19727; S19727.
 DR HSSP: P05067; IQCM.
 DR MGD: MGI:88059; App.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOIDA.
 DR PRINTS: PR00759; BASICPTASE.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 DR Glycoprotein: Amyloid; Neurone; Transmembrane; Signal;
 KW Alternative splicing; Serine protease inhibitor.
 FT SIGNAL 1 17
 FT CHAIN 18 770 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
 FT FT HOMOLOG.
 FT TRANSMEM 18 699 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 700 723 POTENTIAL.
 FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 673 715 EQUIVALENT OF BETA-AMYLOID PROTEIN.
 FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
 FT SITE 759 762 CLATHRIN-BINDING (BY SIMILARITY).
 FT DISULFID 291 341 BY SIMILARITY.
 FT DISULFID 291 341 BY SIMILARITY.
 FT DISULFID 316 337 BY SIMILARITY.
 FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 571 571 E -> V (IN ISOFORM APP(695)).
 FT VARSPLIC 289 364 MISSING (IN ISOFORM APP(695)).
 FT VARSPLIC 346 380 MISSING (IN ISOFORM APP(751)).
 SQ SEQUENCE 770 AA; 86752 MW; 26C50DE0890CAFA7A CRC64;

Query Match Best Local Similarity 100.0%; Score 48; DB 1; Length 770;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10
 DB 666 ISEVKMDAEF 675
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RESULT 6
 A4_RAT STANDARD: PRT: 770 AA.
 ID A4_RAT
 AC P08592;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 16-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog precursor
 DE (Amyloidogenic glycoprotein) (AG).
 GN APP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE=Brain;

RX MEDLINE-68312583; PubMed-2900758;
 RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
 RA Seeburg P.H.;
 RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
 RT in rat brain suggests a role in cell contact."
 RL EMBO J. 7:1365-1370(1988).
 RN [2]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-89183625; PubMed-2648331;
 RA Kang J., Mueller-Hill B.;
 RT "The sequence of the two extra exons in rat preA4";
 RL Nucleic Acids Res. 17:2130-2130(1989).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC CC
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DR EMBL: X07648; CAA30488.1; -;
 DR EMBL: X14066; CAA32229.1; -;
 DR PIR: S00550; S00550.
 DR PIR: S03607; S03607.
 DR HSSP: P05067; IAAP.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOIDA.
 DR PRINTS: PR00759; BASICPTASE.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 KW Alternative splicing; Serine protease inhibitor.
 FT SIGNAL 1 17
 FT CHAIN 18 770 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
 FT FT HOMOLOG.
 FT TRANSMEM 18 699 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 700 723 POTENTIAL.
 FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 673 715 EQUIVALENT OF BETA-AMYLOID PROTEIN.
 FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
 FT SITE 759 762 CLATHRIN-BINDING (BY SIMILARITY).
 FT DISULFID 291 341 BY SIMILARITY.
 FT DISULFID 316 337 BY SIMILARITY.
 FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 571 571 E -> V (IN ISOFORM APP(695)).
 FT VARSPLIC 289 364 MISSING (IN ISOFORM APP(695)).
 SQ SEQUENCE 770 AA; 86704 MW; C26C9D6B82D929A7 CRC64;

Query Match Best Local Similarity 100.0%; Score 48; DB 1; Length 770;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10
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 DB 666 ISEVKMDAEF 675

RESULT 7

A4_PIG STANDARD: PRT: 57 AA.

ID A4_PIG

AC 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [contains: Beta-amyloid

protein (Beta-APP) (A-beta)] (Fragment).

GN APP.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RM [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

peptide in dog, polar bear and five other mammals by cross-species

RT polymerase chain reaction analysis.";

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CC -----

CC EMBL: X56127; CA39592.1; -

DR HSSP: P05067; 1BA4.

DR InterPro: IPR001868; A4_APP.

DR PROSITE: PS00319; A4_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER 1 48

FT CHAIN 6 48

FT DOMAIN <1 33

FT TRANSMEM 34 57

FT NON_TER 57 57

FT SEQUENCE 57 AA; 6172 MW; 84209D88BBA82DFA CRC64;

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CC -----

CC EMBL: X56127; CA39592.1; -

DR HSSP: P05067; 1BA4.

DR InterPro: IPR001868; A4_APP.

DR PROSITE: PS00319; A4_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER 1 48

FT CHAIN 6 48

FT DOMAIN <1 33

FT TRANSMEM 34 57

FT NON_TER 57 57

FT SEQUENCE 57 AA; 6172 MW; 84209D88BBA82DFA CRC64;

CC -----

CC Query Match 91.7%; Score 44; DB 1; Length 57;

CC Best Local Similarity 100.0%; Pred. No. 0.016;

CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC -----

CC OY 2 SEVKMDAEF 10

DB 1 SEVKMDAEF 9

CC -----

CC RESULT 8

CC A4_URSMA STANDARD: PRT: 57 AA.

CC ID A4_URSMA

CC AC 029149;

CC DT 01-NOV-1997 (Rel. 35, Created)

CC DT 01-NOV-1997 (Rel. 35, Last sequence update)

CC DT 30-MAY-2000 (Rel. 39, Last annotation update)

CC DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid

CC RT peptide in dog, polar bear and five other mammals by cross-species

CC RT polymerase chain reaction analysis.";

DE protein (Beta-APP) (A-beta)] (Fragment).

GN APP.

OS Ursus maritimus (Polar bear) (Thalarchos maritimus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.

OX NCBI_TaxID=29073;

RM [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

peptide in dog, polar bear and five other mammals by cross-species

RT polymerase chain reaction analysis.";

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CC -----

CC EMBL: X56128; CA39593.1; -

DR HSSP: P05067; 1AML.

DR InterPro: IPR001868; A4_APP.

DR PROSITE: PS00319; A4_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER 1 48

FT CHAIN 6 48

FT DOMAIN <1 33

FT TRANSMEM 34 57

FT NON_TER 57 57

FT SEQUENCE 57 AA; 6172 MW; 84209D88BBA82DFA CRC64;

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CC -----

CC EMBL: X56128; CA39593.1; -

DR HSSP: P05067; 1AML.

DR InterPro: IPR001868; A4_APP.

DR PROSITE: PS00319; A4_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER 1 48

FT CHAIN 6 48

FT DOMAIN <1 33

FT TRANSMEM 34 57

FT NON_TER 57 57

FT SEQUENCE 57 AA; 6172 MW; 84209D88BBA82DFA CRC64;

CC -----

CC Query Match 91.7%; Score 44; DB 1; Length 57;

CC Best Local Similarity 100.0%; Pred. No. 0.016;

CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC -----

CC OY 2 SEVKMDAEF 10

DB 1 SEVKMDAEF 9

CC -----

CC RESULT 9

CC A4_RABIT STANDARD: PRT: 58 AA.

CC ID A4_RABIT

CC AC 028748;

CC DT 01-NOV-1997 (Rel. 35, Created)

CC DT 01-NOV-1997 (Rel. 35, Last sequence update)

CC DT 16-OCT-2001 (Rel. 40, Last annotation update)

CC DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid

CC protein (Beta-APP) (A-beta)] (Fragment).

GN APP.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RM [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

RT peptide in dog, polar bear and five other mammals by cross-species

RT polymerase chain reaction analysis.";

```

RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -----
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -----
CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL; X56129; CAA39594.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KM Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT NON_TER 1 48
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 91.7%; Score 44; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SEVKMDAEF 10
Db 1 SEVKMDAEF 9

RESULT 10
A4-SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Heart;
RC MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RA "Conservation of the sequence of the Alzheimer's disease amyloid
RA peptide in dog, polar bear and five other mammals by cross-species
RA polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -----
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -----
CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL; X56130; CAA39595.1; -.
DR HSSP; P05067; 1AMT.
DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KM Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT NON_TER 1 48
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 91.7%; Score 44; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SEVKMDAEF 10
Db 1 SEVKMDAEF 9

RESULT 11
YF74_ARCFU STANDARD; PRT; 400 AA.
AC YF74_ARCFU
ID YF74_ARCFU
AD Q28698;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AF1574 precursor.
GN AF1574.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
OX NCBI_TaxID=2234;
[1]
RN SEQUENCE FROM N.A.
RP SFRAIN-VC-16 / DSM 4304 / ATCC 49558;
RC MEDLINE=96049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Kechum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kervatage A.R., Graham D.E., Kyriades N.C.,
RA Fliedemann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Colton M.D., Spriggs T., Arlrich P., Kalne B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RA "The complete genome sequence of the hyperthermophilic, sulphate-
RA reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
CC -----
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CC -----
DR EMBL; AE000994; AAB89681.1; -.
DR TIGR; AF1574; -.
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 23
FT CHAIN 24 400 HYPOTHETICAL PROTEIN AF1574.
SQ SEQUENCE 400 AA; 44117 MW; 5C7BBA00505FD59 CRC64;

```

Query Match 70.8%; Score 34; DB 1; Length 400;
Best Local Similarity 70.0%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
1:111:111
Db 143 ITEVKVKAEE 152

RESULT 12
PGCV_CHICK STANDARD; PRT; 3562 AA.
ID PGCV_CHICK 090953; 090945;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Versican core protein precursor (Large fibroblast proteoglycan)
DE (chondroitin sulfate proteoglycan core protein 2) (PG-M).
GN CPG2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=Limb bud;
RX MEDLINE=93300846; PubMed=8314802;
RA Shinomura T., Nishida Y., Ito K., Kimata K.;
RT "cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan
RT expressed during chondrogenesis in chick limb buds. Alternative
RT spliced multiforms of PG-M and their relationships to versican."
RL J. Biol. Chem. 268:14461-14469(1993).
CC -1- FUNCTION: May play a role in intercellular signaling and in
CC connecting cells with the extracellular matrix. May take part in
CC the regulation of cell motility, growth and differentiation. Binds
CC hyaluronic acid.
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -1- ALTERNATIVE PRODUCTS: At least 2 isoforms; V0 (shown here) and
CC V1: are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Prechondrogenic condensation area of
CC developing limb buds.
CC -1- DEVELOPMENTAL STAGE: Disappears after the cartilage development
CC (by similarity).
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 LINK DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
CC -----
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CC -----
DR EMBL: X60226: CAA42787.1; -;
DR EMBL: D13542: BAA02742.1; -;
DR HSSP: P20693: 1HLJ.
DR InterPro: IPR000152: Asx_hydroxyl.
DR InterPro: IPR000561: EGF-like.
DR InterPro: IPR000742: EGF_2.
DR InterPro: IPR001881: EGF_Ca.
DR InterPro: IPR003599: Ig.
DR InterPro: IPR003006: Ig_MHC.
DR InterPro: IPR000538: Link.
DR InterPro: IPR000436: Sushi_SCR_CCP.
DR InterPro: IPR001304: lectin_c.
DR Pfam: PF000008: EGF_2.
DR Pfam: PF00047: igf_1.
DR Pfam: PF00059: lectin_c; 1.

DR Pfam: PF000084: sushi; 1.
DR Pfam: PF00193: Xlink; 2.
DR ProDom: PD000918: Link; 2.
DR SMART: SM00032: CCP; 1.
DR SMART: SM00034: CLECT; 1.
DR SMART: SM00179: EGF_Ca; 1.
DR SMART: SM00001: EGF_Like; 1.
DR SMART: SM00409: IG; 1.
DR SMART: SM00445: LINK; 2.
DR PROSITE: PS00010: ASX_HYDROXYL; 1.
DR PROSITE: PS00022: EGF_1; 2.
DR PROSITE: PS01186: EGF_2; 1.
DR PROSITE: PS01187: EGF_Ca; 2.
DR PROSITE: PS01241: LINK; 2.
DR PROSITE: PS00615: C-TYPE LECTIN_1; 1.
DR PROSITE: PS50041: C-TYPE LECTIN_2; 1.
DR GlycoProtein: Proteoglycan; Lectin; Extracellular matrix; Sushi;
KW Signal: Repeat: EGF-like domain; Calcium; Immunoglobulin domain;
KW Hyaluronic acid; Alternative splicing.
KW SIGNAL 1 26
FT CHAIN 27 3562
FT DOMAIN 37 136
FT DOMAIN 166 243
FT DOMAIN 264 345
FT DOMAIN 3254 3290
FT DOMAIN 3292 3328
FT DOMAIN 3341 3455
FT DOMAIN 3460 3518
FT DISULFID 44 129
FT DISULFID 171 242
FT DISULFID 195 216
FT DISULFID 269 344
FT DISULFID 293 314
FT DISULFID 3258 3269
FT DISULFID 3263 3278
FT DISULFID 3280 3289
FT DISULFID 3296 3307
FT DISULFID 3301 3316
FT DISULFID 3318 3327
FT DISULFID 3334 3345
FT DISULFID 3362 3454
FT DISULFID 3430 3446
FT DISULFID 3461 3504
FT DISULFID 3490 3517
FT CARBOHYD 163 163
FT CARBOHYD 235 235
FT CARBOHYD 329 329
FT CARBOHYD 529 529
FT CARBOHYD 709 709
FT CARBOHYD 948 948
FT CARBOHYD 1409 1409
FT CARBOHYD 1479 1479
FT CARBOHYD 1523 1523
FT CARBOHYD 1530 1530
FT CARBOHYD 1625 1625
FT CARBOHYD 1751 1751
FT CARBOHYD 1988 1988
FT CARBOHYD 2088 2088
FT CARBOHYD 2089 2089
FT CARBOHYD 2507 2507
FT CARBOHYD 2642 2642
FT CARBOHYD 2679 2679
FT CARBOHYD 2748 2748
FT CARBOHYD 2762 2762
FT CARBOHYD 3069 3069
FT CARBOHYD 3194 3194
FT CARBOHYD 3232 3232
FT CARBOHYD 3545 3545
FT VARSPLIC 485 1411
SQ SEQUENCE 3562 AA; 388078 MM; 98C56E8BC160222 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 3562;
Best Local Similarity 66.7%; Pred. No. 1,4e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SEVKMDAEF 10
1:|||||

Db 1709 STIKLDAEF 1717

RESULT 13

TS1_STREF
ID TS1_STREF STANDARD: PRT; 269 AA.

AC 052512;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Type II restriction enzyme SfiI (EC 3.1.21.4) (Endonuclease SfiI)
(/R.SfiI).

CN SfiI.

OS Streptomyces fimbriatus.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=68197;
RN [1]
RN SEQUENCE FROM N.A.
RA van Cott E.M., Moran L.S., Slatko B.E., Wilson G.G.;
RT "Characterization of the SfiI restriction and modification genes."
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE GGCCNNNNNGGCC
CC AND CLEAVES BEFORE N-9.
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC specific double-stranded fragments with terminal 5'-phosphates.
CC -----
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CC -----
DR EMBL; AF039750; AAB95365.1; -
DR REBASE; 1655; SfiI.
KM Hydrolyase: Endonuclease; Nuclease; Restriction system.
SQ SEQUENCE 269 AA; 31044 MW; 3C48A99BAA5055EA CRC64;

Query Match 66.7%; Score 32; DB 1; Length 269;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SEVKMDAEF 10
1:|||||

Db 115 SQLPMDAEF 123

RESULT 14

BCPA_CHLIT
ID BCPA_CHLIT STANDARD: PRT; 354 AA.

AC 046135;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bacteriochlorophyll A protein (Bchl a protein) (BCP) (Fenna-Matthews-
DE Olson protein) (FMO-protein) (Fragment).
GN FMOA.
OS Chlorobium limicola f.sp. thisulfatophilum.
OC Bacteria; Green sulfur bacteria; Chlorobium.
OX NCBI_TaxID=115852;
RN [1]
RN SEQUENCE FROM N.A.
RA MEDLINE=95352646; PubMed=7626630;
RA Hager-Braun C., Xie D.L., Jarsch U., Herold E., Butner M.,
RA Zimmermann R., Deutzmann R., Hauska G., Nelson N.;
RT "Stable photobleaching of P840 in Chlorobium reaction center
preparations: presence of the 42-kDa bacteriochlorophyll a protein

RT and a 17-kDa polypeptide.";
RL Biochemistry 34:9617-9624(1995).
CC -1- FUNCTION: INTERMEDIARY IN THE TRANSFER OF EXCITATION ENERGY FROM
CC THE CHLOROPHYLL TO THE REACTION CENTERS.
CC -1- SUBUNIT: HOMOTRIMER. EACH SUBUNIT CONTAINS 7 MOLECULES OF
CC BACTERIOCHLOROPHYLL A.
CC -----
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CC -----
DR EMBL; X83529; CAA58510.1; -
DR HSSP; Q46393; IKS.A.
DR InterPro; IPR003426; Bchl_A.
DR Pfam; PF02327; Bchl_A; 1.
KM Electron transport; Photosynthesis; Reaction center; Magnesium;
KW Bacteriochlorophyll.
FT NON_TER 1 1
FT BINDING 99 99 BACTERIOCHLOROPHYLL A, 1 (BY SIMILARITY)
FT BINDING 134 134 BACTERIOCHLOROPHYLL A, 6 (BY SIMILARITY)
FT BINDING 278 278 BACTERIOCHLOROPHYLL A, 4 (BY SIMILARITY)
FT BINDING 285 285 BACTERIOCHLOROPHYLL A, 7 (BY SIMILARITY)
FT BINDING 286 286 BACTERIOCHLOROPHYLL A, 3 (BY SIMILARITY)
SQ SEQUENCE 354 AA; 39243 MW; F4DAD565BDCDB1B CRC64;

Query Match 66.7%; Score 32; DB 1; Length 354;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EVKMDAEF 10
1:|||||

Db 254 EVKMDAEF 261

RESULT 15

BCPA_CHLITE
ID BCPA_CHLITE STANDARD: PRT; 365 AA.

AC 046393;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Bacteriochlorophyll A protein (Bchl a protein) (BCP) (Fenna-Matthews-
DE Olson protein) (FMO-protein).
GN FMOA.
OS Chlorobium tepidum.
OC Bacteria; Green sulfur bacteria; Chlorobium.
OX NCBI_TaxID=1097;
RN [1]
RN SEQUENCE FROM N.A.
RA Dracheva S., Williams J.A.C., Blankenship R.E.;
RT "Cloning and sequencing of the FMO-protein gene from Chlorobium
RT tepidum."
RL (in) Murata N. (eds.);
RL Research in photosynthesis, pp.2:53-56, Kluwer Academic Publishers,
RL Dordrecht (1992).
RN [2]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=97415773; PubMed=9268671.
RA LI Y.F., Zhou W., Blankenship R.E., Allen J.P.;
RT "Crystal structure of the bacteriochlorophyll a protein from
RT Chlorobium tepidum."
RL J. Mol. Biol. 271:456-471(1997).
CC -1- FUNCTION: INTERMEDIARY IN THE TRANSFER OF EXCITATION ENERGY FROM
CC THE CHLOROPHYLL TO THE REACTION CENTERS.
CC -1- SUBUNIT: HOMOTRIMER. EACH SUBUNIT CONTAINS 7 MOLECULES OF
CC BACTERIOCHLOROPHYLL A.
CC -----
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CC -----
 DR EMBL: L13700: AAA23111.1; -.
 DR PDB: 1KSA: 25-FER-98.
 DR InterPro: IPR003426; Bchl_A.
 DR Pfam: PF02327; Bchl_A: 1.
 KW Electron transport; Photosynthesis; Reaction center; Magnesium;
 KW 3D-structure; Bacteriochlorophyll.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT BINDING 110 110 BACTERIOCHLOROPHYLL A, 1.
 FT BINDING 145 145 BACTERIOCHLOROPHYLL A, 6.
 FT BINDING 289 289 BACTERIOCHLOROPHYLL A, 4.
 FT BINDING 296 296 BACTERIOCHLOROPHYLL A, 7.
 FT BINDING 297 297 BACTERIOCHLOROPHYLL A, 3.
 SQ SEQUENCE 365 AA; 40163 MW; EB48DFE24DF6A780 CRC64;

Query Match

Best Local Similarity 66.7%; Score 32; DB 1; Length 365;
 Best Local Similarity 75.0%; Pred. No. 32;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EYKMDAEF 10
 |||:|
 DB 265 EVKVDGEF 272

Search completed: October 29, 2002, 10:27:27
 Job time : 6 secs

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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:11 ; Search time 18 Seconds
(without alignments)
96.108 Million cell updates/sec

Title: US-09-580-018-3
Perfect score: 48
Sequence: 1 ISEVKMDAER 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mmc:*
9: sp_organelle:*
10: sp_phase:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_rvivirus:*
17: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	100.0	79	11	O35463	O35463 Cricetus
2	48	100.0	82	4	P78438	P78438 homo sapien
3	48	100.0	82	4	Q16014	Q16014 homo sapien
4	48	100.0	82	4	Q16019	Q16019 homo sapien
5	48	100.0	82	4	Q16020	Q16020 homo sapien
6	48	100.0	607	11	O99K32	O99K32 mus musculi
7	48	100.0	695	6	O95KN7	O95KN7 macaca fasc
8	48	100.0	695	11	P97487	P97487 mus musculi
9	48	100.0	695	11	O60496	O60496 cavia sp. p
10	48	100.0	770	6	O9TU10	O9TU10 sus scrofa
11	47	97.9	534	13	O93296	O93296 gallus gall
12	47	97.9	569	13	O9PVL1	O9PVL1 gallus gall
13	47	97.9	695	13	O9DCJ8	O9DCJ8 gallus gall
14	47	97.9	751	13	O9DCJ7	O9DCJ7 gallus gall
15	42	87.5	693	13	O98SG0	O98SG0 xenopus lae
16	42	87.5	693	13	O98SF9	O98SF9 xenopus lae

17	42	87.5	747	13	O91963	O91963 xenopus. ap
18	37	77.1	423	2	O52379	O52379 raietonia s
19	37	77.1	423	2	O45693	O45693 burkholderi
20	36	75.0	630	2	O93IK4	O93IK4 vibrio sp.
21	34	70.8	142	5	O16896	O16896 caenorhabdi
22	34	70.8	317	17	O962R2	O962R2 sulfoblob
23	34	70.8	699	13	O57394	O57394 narke japon
24	34	70.8	700	16	O9K679	O9K679 bacillus ha
25	33	68.8	242	10	O9C7X4	O9C7X4 arabidopsis
26	33	68.8	389	17	O9HR27	O9HR27 halobacteri
27	33	68.8	626	2	O56633	O56633 vibrio chol
28	33	68.8	626	2	O9AGW8	O9AGW8 vibrio chol
29	33	68.8	626	16	O9KT07	O9KT07 vibrio chol
30	32	66.7	143	4	O9H935	O9H935 homo sapien
31	32	66.7	261	16	O25173	O25173 homo sapien
32	32	66.7	261	16	O9ZKH1	O9ZKH1 helicobacte
33	32	66.7	266	5	O965M5	O965M5 caenorhabdi
34	32	66.7	282	5	O02335	O02335 caenorhabdi
35	32	66.7	338	2	O9AL67	O9AL67 chlorobium
36	32	66.7	350	2	O9AL73	O9AL73 chlorobium
37	32	66.7	350	2	O9AL69	O9AL69 chlorobium
38	32	66.7	350	2	O9AL72	O9AL72 chlorobium
39	32	66.7	400	2	O52295	O52295 shigella fl
40	32	66.7	405	4	O9BU21	O9BU21 homo sapien
41	32	66.7	426	17	O9V2P8	O9V2P8 pyrococcus
42	32	66.7	470	16	O9RYP8	O9RYP8 delinococcus
43	32	66.7	539	4	O9NWD6	O9NWD6 homo sapien
44	32	66.7	539	4	O9NWA5	O9NWA5 homo sapien
45	32	66.7	614	4	O96SR8	O96SR8 homo sapien

ALIGNMENTS

RESULT 1
O35463 PRELIMINARY: PRT: 79 AA.
ID O35463
AC O35463;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).
GN BETA APP.
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCB1_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Sambamurti K., Plinix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF030413; AAB86608.1; -.
DR HSSP; P05067; 1BA4.
FT NON_TER 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 8538 MW; 37FE2C6C3BF3F597 CRC64;
Query Match 100.0%; Score 48; DB 11; Length 79;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ISEVKMDAER 10
DB 15 ISEVKMDAER 24
RESULT 2
P78438 PRELIMINARY: PRT: 82 AA.
AC P78438;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)

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DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [2]
RP SEQUENCE OF 19-48 FROM N.A.
RX MEDLINE=87120329; PubMed=2949367;
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neye R.L.;
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
RT linkage near the Alzheimer locus.";
RL Science 235:880-884(1987).
RN [3]
RP SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE=93035397; PubMed=1415269;
RA Kamino K., Orr H.T., Payami H., Wijman E.M., Alonso M.E., Pulst S.M.,
RA Anderson L., O'dahl S., Nemens E., White J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease
RT kindreds for the APP gene region.";
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL: M29270; AAAS1768.1; -.
DR EMBL: M29269; AAAS1768.1; JOINED.
DR EMBL: S45136; AAB23646.1; -.
DR HSSP: P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match
Best Local Similarity 100.0%; Score 48; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
DB 11 ISEVKMDAEF 20

RESULT 3
ID Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S60721; AAB26263.2; -.
DR HSSP: P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8972 MW; F534AAB3EA9230A CRC64;

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Query Match
Best Local Similarity 100.0%; Score 48; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
DB 12 ISEVKMDAEF 21

RESULT 4
ID Q16019 PRELIMINARY; PRT; 82 AA.
AC Q16019;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S61380; AAB26264.2; -.
DR HSSP: P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match
Best Local Similarity 100.0%; Score 48; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
DB 12 ISEVKMDAEF 21

RESULT 5
ID Q16020 PRELIMINARY; PRT; 82 AA.
AC Q16020;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S61383; AAB26265.2; -.
DR HSSP: P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match
Best Local Similarity 100.0%; Score 48; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 ISEVKMDAEF 10
 |||||||
 Db 12 ISEVKMDAEF 21

RESULT 6

099K32 PRELIMINARY; PRT; 607 AA.
 AC 099K32;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HYPOTHEtical 68.4 KDA PROTEIN (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD. CROSS
 RC TISSUE;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC005490; AAH05490.1; -.
 DR HSSP; P05067; IAPP.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 KM Hypothetical protein; Serine protease inhibitor.
 FT NON_TER
 FT SEQUENCE 607 AA; 68391 MW; BF80221ACBA7D172 CRC64;
 SQ
 Query Match 100.0%; Score 48; DB 11; Length 607;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10
 |||||||
 Db 503 ISEVKMDAEF 512

RESULT 7
 095KN7 PRELIMINARY; PRT; 695 AA.
 AC 095KN7;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE AMYLOID B-PROTEIN PRECURSOR.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CEREBELLUM;
 RX MEDLINE-91273117; PubMed-1905108;
 RX Podlinsky M.B., Tolian D.R., Selkoe D.J.;
 RA "Homology of the amyloid beta protein precursor in monkey and human
 RT supports a primate model for beta amyloidosis in Alzheimer's
 disease";
 RL Am. J. Pathol. 138:1423-1435(1991).
 DR EMBL; M58727; AAA36829.1; -.
 FT SIGNAL 1 17 POTENTIAL.

FT CHAIN 597 636 POTENTIAL.
 SQ SEQUENCE 695 AA; 78663 MW; 4FE6EA0139F969D56 CRC64;

Query Match 100.0%; Score 48; DB 6; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10
 |||||||
 Db 591 ISEVKMDAEF 600

RESULT 8

P97487 PRELIMINARY; PRT; 695 AA.
 AC P97487; P97942;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HIPPOCAMPAL AMYLOID PROTEIN.
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SAMP8; TISSUE=HIPPOCAMPUS;
 RA Flood J.F., Kumar V.B., Sasser T., Morley J.E.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 581-662 FROM N.A.
 RC STRAIN=129SV;
 RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capechi M.,
 RA Loring J.F., Goate A.M.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U84012; AAB41502.1; -.
 DR EMBL; U82624; AAB40919.1; -.
 DR HSSP; P05067; IMMP.
 DR MGD; MGI:88059; APP.
 DR InterPro; IPR001868; A4_APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_EXTRA; 1.
 SQ SEQUENCE 695 AA; 78414 MW; 9A5FBE2ED261236E CRC64;
 SQ
 Query Match 100.0%; Score 48; DB 11; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10
 |||||||
 Db 591 ISEVKMDAEF 600

RESULT 9
 060496 PRELIMINARY; PRT; 695 AA.
 ID 060496;
 AC 060496;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PUTATIVE AMYLOID PRECURSOR PROTEIN.
 OS Cavia sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
 NCBI_TaxID=10143;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE-97236426; PubMed-9116031;

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RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL; X97631; CA66230.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 100.0%; Score 48; DB 11; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
Db 591 ISEVKMDAEF 600

RESULT 10
Q9TUI0 PRELIMINARY; PRT; 770 AA.
AC Q9TUI0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid Precursor Protein 770.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032550; BAAB4580.1; -.
DR HSSP; P05067; 1AAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB28CC583E CRC64;

Query Match 100.0%; Score 48; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
Db 666 ISEVKMDAEF 675

RESULT 11
Q93296 PRELIMINARY; PRT; 534 AA.
AC Q93296;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

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DE AMYLOID PROTEIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE; 98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL; AF042098; AAC25052.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 97.9%; Score 47; DB 13; Length 534;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
Db 430 VSEVKMDAEF 439

RESULT 12
Q9PVL1 PRELIMINARY; PRT; 569 AA.
AC Q9PVL1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
GN App.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Coulson E.J., Paliaga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function.";
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12698.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0ABBB851863A19D CRC64;

Query Match 97.9%; Score 47; DB 13; Length 569;
Best Local Similarity 90.0%; Pred. No. 0.23;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
Db 466 VSEVKMDAEF 475

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RESULT 13
Q9DGI8      PRELIMINARY;      PRT;      695 AA.
ID   Q9DGI8
AC   Q9DGI8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DE   01-MAR-2001 (TrEMBLrel. 16, last sequence update)
DE   01-DEC-2001 (TrEMBLrel. 19, last annotation update)
OS   BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
OC   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms."
RL   Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR   EMBL; AF289218; AAG00593.1;
DR   HSSP; P05067; IBA4.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
SQ   SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match          97.9%; Score 47; DB 13; Length 695;
Best Local Similarity 90.0%; Pred. No. 0.28;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
DB 591 VSEVKMDAEF 600

RESULT 14
Q9DGI7      PRELIMINARY;      PRT;      751 AA.
ID   Q9DGI7;
AC   Q9DGI7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DE   01-MAR-2001 (TrEMBLrel. 16, last sequence update)
DE   01-DEC-2001 (TrEMBLrel. 19, last annotation update)
DE   BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms."
RL   Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR   EMBL; AF289219; AAG00594.1;
DR   HSSP; P05067; IBA4.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU_1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR   Serine protease inhibitor.
SQ   SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match          97.9%; Score 47; DB 13; Length 751;
Best Local Similarity 90.0%; Pred. No. 0.3;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
DB 647 VSEVKMDAEF 656

RESULT 15
Q98SG0      PRELIMINARY;      PRT;      693 AA.
ID   Q98SG0;
AC   Q98SG0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DE   01-JUN-2001 (TrEMBLrel. 17, last sequence update)
DE   01-DEC-2001 (TrEMBLrel. 19, last annotation update)
DE   BETA-AMYLOID PRECURSOR PROTEIN A.
OS   APP.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RT   van den Hurk W.H.;
RT   Thesis (2001); Department of Biological Sciences,
RL   University of Nijmegen, Nijmegen, Netherlands.
DR   EMBL; AJ296150; CAC37193.1;
DR   HSSP; P05067; IH23.
DR   InterPro; IPR001868; A4_APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   Signal.
FT   SIGNAL.
SQ   SEQUENCE 693 AA; 78568 MW; CAF1DF655C1A853 CRC64;

Query Match          87.5%; Score 42; DB 13; Length 693;
Best Local Similarity 80.0%; Pred. No. 3;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
DB 589 ISEVKMDSEY 598

Search completed: October 29, 2002, 10:29:40
Job time : 20.1429 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:56 : Search time 9 seconds
(without alignments)
27.140 Million cell updates/sec

Title: US-09-580-018-3

Perfect score: 48

Sequence: 1 ISEYKMDAEF 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents-AA:*

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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/PCYUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	48	100.0	11	5	PCT-US94-07043A-7
2	48	100.0	12	5	PCT-US94-07043A-2
3	48	100.0	16	5	PCT-US94-07043A-1
4	48	100.0	27	1	US-08-141-3324-11
5	48	100.0	27	1	US-08-541-902-11
6	48	100.0	45	1	US-08-462-859A-5
7	48	100.0	45	1	US-08-123-659A-5
8	48	100.0	45	1	US-08-464-247A-5
9	48	100.0	45	1	US-08-464-248A-5
10	48	100.0	58	1	US-08-371-930-25
11	48	100.0	58	5	PCT-US94-01712-25
12	48	100.0	63	1	US-08-462-859A-3
13	48	100.0	63	1	US-08-462-859A-4
14	48	100.0	63	1	US-08-123-659A-3
15	48	100.0	63	1	US-08-123-659A-4
16	48	100.0	63	1	US-08-464-247A-3
17	48	100.0	63	1	US-08-464-247A-4
18	48	100.0	63	1	US-08-464-248A-3
19	48	100.0	63	1	US-08-464-248A-4
20	48	100.0	105	2	US-08-729-345-1
21	48	100.0	117	2	US-08-729-345-3
22	48	100.0	152	6	5187153-4
23	48	100.0	162	6	5220013-4
24	48	100.0	162	6	5223482-4
25	48	100.0	264	1	US-07-990-893-5
26	48	100.0	487	1	US-08-462-859A-9
27	48	100.0	487	1	US-08-123-659A-9

28	48	100.0	487	1	US-08-464-247A-9	Sequence 9, Appl
29	48	100.0	487	1	US-08-464-248A-9	Sequence 9, Appl
30	48	100.0	492	1	US-08-462-859A-7	Sequence 7, Appl
31	48	100.0	492	1	US-08-123-659A-7	Sequence 7, Appl
32	48	100.0	492	1	US-08-464-247A-7	Sequence 7, Appl
33	48	100.0	492	1	US-08-464-248A-7	Sequence 7, Appl
34	48	100.0	537	2	US-08-453-552-4	Sequence 4, Appl
35	48	100.0	537	2	US-08-710-637-4	Sequence 4, Appl
36	48	100.0	537	5	PCT-US93-00907-4	Sequence 4, Appl
37	48	100.0	656	1	US-08-371-930-23	Sequence 23, Appl
38	48	100.0	656	5	PCT-US94-01712-23	Sequence 23, Appl
39	48	100.0	676	1	US-08-371-930-24	Sequence 24, Appl
40	48	100.0	676	5	PCT-US94-01712-24	Sequence 24, Appl
41	48	100.0	694	1	US-08-339-152A-18	Sequence 18, Appl
42	48	100.0	694	2	US-08-007-999B-5	Sequence 5, Appl
43	48	100.0	694	2	US-08-689-276A-5	Sequence 5, Appl
44	48	100.0	695	1	US-08-371-930-27	Sequence 27, Appl
45	48	100.0	695	1	US-08-123-702-2	Sequence 2, Appl

ALIGNMENTS

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RESULT 1
PCT-US94-07043A-7
: Sequence 7, Application PC/TUS9407043A
:
: GENERAL INFORMATION:
: APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,
: APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard
: TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC
: TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Miles Inc.
: STREET: 400 Morgan Lane
: CITY: West Haven
: STATE: Connecticut
: COUNTRY: USA
: ZIP: 06516
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
: COMPUTER: Sharp PC 4600
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: Wordperfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/07043A
: FILING DATE: June 21, 1994
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/10889
: FILING DATE: November 12, 1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/995,660
: FILING DATE: December 16, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/880,914
: FILING DATE: May 11, 1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Pamela A. Simonton
: REGISTRATION NUMBER: 31,060
: REFERENCE/DOCKET NUMBER: MTI 224.3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (203) 937-2340
: TELEFAX: (203) 937-2795
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 11 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: PCT-US94-07043A-7
:
: Query Match 100.0%; Score 48; DB 5; Length 11;
: Best Local Similarity 100.0%; Pred. No. 0.00057;
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10
| | | | | | | | | |
Db 1 ISEVKMDAEF 10

RESULT 2
PCT-US94-07043A-2
Sequence 2, Application PC/TUS9407043A
GENERAL INFORMATION:
APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,
APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard
TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC
TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miles Inc.
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
COMPUTER: Sharp PC 4600
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07043A
FILING DATE: June 21, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10889
FILING DATE: November 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/995,660
FILING DATE: December 16, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/880,914
FILING DATE: May 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Pamela A. Simonton
REGISTRATION NUMBER: 31,060
REFERENCE/DOCKET NUMBER: MTI 224.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 937-2340
TELEFAX: (203) 937-2795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-07043A-2

Query Match 100.0%; Score 48; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10
| | | | | | | | | |
Db 1 ISEVKMDAEF 10

RESULT 3
PCT-US94-07043A-1
Sequence 1, Application PC/TUS9407043A
GENERAL INFORMATION:
APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,
APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard
TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC
TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE
NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
ADDRESSEE: Miles Inc.
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
COMPUTER: Sharp PC 4600
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07043A
FILING DATE: June 21, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10889
FILING DATE: November 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/995,660
FILING DATE: December 16, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/880,914
FILING DATE: May 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Pamela A. Simonton
REGISTRATION NUMBER: 31,060
REFERENCE/DOCKET NUMBER: MTI 224.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 937-2340
TELEFAX: (203) 937-2795
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-07043A-1

Query Match 100.0%; Score 48; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10
| | | | | | | | | |
Db 1 ISEVKMDAEF 10

RESULT 4
US-08-141-324-11
Sequence 11, Application US/08141324
Patent No. 5475097
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Nadine
APPLICANT: Pike, Robert N.
TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,324
FILING DATE: 21-OCT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 44-93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
TELEFAX: 303-499-8080
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-141-324-11

Query Match Best Local Similarity 100.0%; Score 48; DB 1; Length 27;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10
|||||
DB 3 ISEVKMDAEF 12

RESULT 5
US-08-541-902-11
Sequence 11, Application US/08541902
Patent No. 5707620
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Nadine
APPLICANT: Pike, Robert N.
TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
TITLE OF INVENTION: Protease
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,902
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/141,324
FILING DATE: 21-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 44-93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
TELEFAX: 303-499-8080
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-541-902-11

Query Match Best Local Similarity 100.0%; Score 48; DB 1; Length 27;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10
|||||
DB 3 ISEVKMDAEF 12

RESULT 6
US-08-462-859A-5
Sequence 5, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-5

Query Match Best Local Similarity 100.0%; Score 48; DB 1; Length 45;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISEVKMDAEF 10
|||||
DB 4 ISEVKMDAEF 13

RESULT 7
US-08-123-659A-5
Sequence 5, Application US/08123659A
Patent No. 5656477

GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5656477e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/123,659A
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-5

Query Match 100.0%; Score 48; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
|||||
DB 4 ISEVKMDAEF 13

RESULT 8
US-08-464-247A-5
Sequence 5, Application US/08464247A
Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/464,247A
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-5

Query Match 100.0%; Score 48; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
|||||
DB 4 ISEVKMDAEF 13

RESULT 9
US-08-464-248A-5
Sequence 5, Application US/08464248A
Patent No. 5703209
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5703209e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/464,248A
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-5

Query Match 100.0%; Score 48; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
|||||
DB 4 ISEVKMDAEF 13

RESULT 10

US-08-371-930-25
Sequence 25, Application US/08371930
Patent No. 5578451
GENERAL INFORMATION:
APPLICANT: Nishimoto, Ikuo
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,930
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/019,208
FILING DATE: February 18, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/154001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 58
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-371-930-25

Query Match 100.0%; Score 48; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
|||||
DB 41 ISEVKMDAEF 50

RESULT 11

PCT-US94-01712-25
Sequence 25, Application PC/TUS9401712
GENERAL INFORMATION:
APPLICANT: Nishimoto, Ikuo
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/019,208
FILING DATE: February 18, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/154001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 58
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US94-01712-25

Query Match 100.0%; Score 48; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
|||||
DB 41 ISEVKMDAEF 50

RESULT 12
US-08-462-859A-3
Sequence 3, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-3

Query Match 100.0%; Score 48; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
|||||
DB 4 ISEVKMDAEF 13

RESULT 13
US-08-462-859A-4
Sequence 4, Application US/08462859A
Patent No. 5652092

GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: NO. 5652092el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-4

Query Match 100.0%; Score 48; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
|||||
DB 4 ISEVKMDAEF 13

RESULT 14
US-08-123-659A-3
Sequence 3, Application US/08123659A
Patent No. 5656477

GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.

TITLE OF INVENTION: NO. 5656477el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-3

Query Match 100.0%; Score 48; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISEVKMDAEF 10
|||||
DB 4 ISEVKMDAEF 13

RESULT 15
US-08-123-659A-4
Sequence 4, Application US/08123659A
Patent No. 5656477
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: NO. 5656477el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.

REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-4

Query Match 100.0%; Score 48; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ISEVKMDAEF 10
| | | | | | | | | |
Db 4 ISEVKMDAEF 13

Search completed: October 29, 2002, 10:32:07
Job time : 10 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:21 ; Search time 23.1429 Seconds
(without alignments)
47.995 Million cell updates/sec

Title: US-09-580-018-4

Perfect score: 49

Sequence: 1 SEVKMDAEPK 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_032802.*
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11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	49	100.0	10	13	AA24261	Human amyloid pr
2	49	100.0	10	21	AA69703	Beta-APP alpha-sec
3	49	100.0	10	22	AAE10654	Human wild-type AP
4	49	100.0	10	22	AAE06899	Human amyloid prec
5	49	100.0	10	22	AAU06628	Asp2 recognition s
6	49	100.0	10	22	AAU07227	Human beta-amyloid
7	49	100.0	10	22	AAE02606	Human wild-type AP
8	49	100.0	10	22	AAE66574	Synthetic peptide
9	49	100.0	10	22	AAH46208	Human APP derived
10	49	100.0	10	22	AAE61336	Synthetic peptide f
11	49	100.0	11	22	AAE75143	APP beta-secretase

12	49	100.0	11	22	AAE75144	ASP 1 substrate se
13	49	100.0	11	22	AAE97468	ASP2 substrate w11
14	49	100.0	13	21	AAW70869	Beta-amyloid pepti
15	49	100.0	16	21	AAE06315	Human beta-amyloid
16	49	100.0	16	21	AAE06317	Human beta-amyloid
17	49	100.0	18	22	AAE00608	Beta-amyloid precu
18	49	100.0	20	21	AAE69713	Beta-APP alpha-sec
19	49	100.0	23	22	AAE75147	ASP 1 substrate se
20	49	100.0	23	22	AAE97473	ASP2 substrate w11
21	49	100.0	33	20	AAE98002	Amyloid precursor
22	49	100.0	39	21	AAE69717	Beta-APP alpha-sec
23	49	100.0	45	18	AAE26512	Amyloid precursor
24	49	100.0	45	18	AAE26592	Amyloid precursor
25	49	100.0	45	19	AAW44748	APP-REP 751 (BAP d
26	49	100.0	45	19	AAW42977	Deletion beta-amylo
27	49	100.0	53	16	AAE64168	Variant beta-amylo
28	49	100.0	54	21	AAE32126	Amyloid-beta precu
29	49	100.0	57	21	AAE10910	Human amyloid prec
30	49	100.0	58	15	AAE58937	Amyloid precursor
31	49	100.0	63	18	AAE26511	Amyloid precursor
32	49	100.0	63	18	AAE26591	Amyloid precursor
33	49	100.0	63	19	AAW44747	APP-REP 751 BAP pe
34	49	100.0	63	19	AAW44746	APP-REP 751 (BAP E
35	49	100.0	63	19	AAW42975	Beta-amyloid pepti
36	49	100.0	63	19	AAW42976	Beta-amyloid pepti
37	49	100.0	67	19	AAW71377	Peptide derived fr
38	49	100.0	93	22	AAE19083	Novel human diagno
39	49	100.0	104	19	AAW51100	Amino acid sequenc
40	49	100.0	112	17	AAE93556	Familial Alzheimer
41	49	100.0	115	20	AAW97999	London-PAD APP pol
42	49	100.0	117	19	AAW51102	Flag-amyloid prote
43	49	100.0	162	9	AAE83151	Deduced sequence 1
44	49	100.0	162	12	AAE10023	Beta-amyloid-relat
45	49	100.0	162	14	AAE37863	Deduced from clone

ALIGNMENTS

RESULT 1	AA24261	standard; protein; 10 AA.
XX	AA24261;	
XX	09-NOV-1992 (first entry)	
XX	Human amyloid protease substrate sequence #1.	
XX	Alzheimer's disease; beta amyloid precursor protein; APP; zinc;	
XX	metalloprotease; hAP; protease inhibitor; APP592-601	
XX	Synthetic.	
XX	Key	Location/Qualifiers
XX	Modified-site	1
XX		/note="Acetylated-Ser"
XX	W09207068-A.	
XX	30-APR-1992.	
XX	04-OCT-1991;	91WO-US07290.
XX	05-OCT-1990;	90US-0594122.
XX	30-SEP-1991;	91US-0766351.
XX	(ATHE-) ATHENA NEUROSCIENCES INC.	
XX	(ELIL) LILLY & CO ELI.	
XX	Dorey HF, Johnstone EM, Little SP, McConlogue L, Seubert PA;	
XX	Sinha S;	

DR WPI: 1992-167148/20.
XX Human amyloidin protease - used for cleaving Met-Asp bond in
PT amyloid-like substrate for identifying protease inhibitors
XX
PS Claim 1; Page 52; 62pp; English.
XX
CC Claimed human amyloidin protease is defined by its ability to
CC cleave the Met-Asp bond of this synthetic substrate. The substrate,
CC which corresponds to residues 592 to 601 of the 695 amino acid APP,
CC can be used in an assay for identifying inhibitors of proteases
CC which cleave Met-Asp bonds, e.g. amyloidin, human skin chymase or
CC rat mast cell protease I or II.
CC See AAR24260-3, AAR24266-7 and AAQ24875-Q24887.
CC
XX
SQ Sequence 10 AA:

Query Match 100.0%; Score 49; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEFR 10
| | | | | | | | | |
Db 1 SEVKMDAEFR 10

RESULT 2
AA69703
ID AAY69703 standard; peptide: 10 AA.
XX
AC AAY69703;
XX
DT 11-APR-2000 (first entry)
XX
XX Beta-APP alpha-secretase substrate [KMD]-APP(-5,+5).
DE
XX Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
KM cleavage site; beta-secretase; neurodegenerative disease;
KM Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN MO9964587-A1.
XX
PD 16-DEC-1999.
XX
PF 04-JUN-1999; 99WO-FR01326.
XX
PR 05-JUN-1998; 98FR-0007068.
PR 31-MAR-1999; 99US-0122599.
XX
XX (RHON) RHONE-POULENC RORER SA.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
XX Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
PI
XX WPI: 2000-097537/08.
DR
XX Polypeptide with beta-secretase activity, specific for wild-type
PT amyloid precursor protein, useful in treating Alzheimer's disease -
XX
PS Example 3; Page 24; 44pp; French.
XX
CC Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
CC novel polypeptide with beta-secretase activity that can cleave
CC specifically the natural beta-amyloid precursor protein (bAPP). Normal
CC cleavage of the protein occurs between amino acids Met596-Asp597 and
CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
CC polypeptide is used to identify agents that interact specifically with
CC it. These agents regulate metabolism of APP, particularly they slow down
CC or reduce production of beta-amyloid, so can be used to treat
CC neurodegenerative diseases, particularly Alzheimer's disease.
CC

SQ Sequence 10 AA:

Query Match 100.0%; Score 49; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEFR 10
| | | | | | | | | |
Db 1 SEVKMDAEFR 10

RESULT 3
AAE10654
ID AAE10654 standard; peptide: 10 AA.
XX
AC AAE10654;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human wild-type APP beta-secretase peptide, PHA-95812E.
XX
XX Human; aspartyl protease 1; Aspl; amyloid precursor protein;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW APP beta-secretase peptide.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Cleavage-site 5..6
XX
PN GB2357767-A.
XX
PD 04-JUL-2001.
XX
XX 22-SEP-2000; 2000GB-0023315.
PF
XX 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX
XX (PHAA) PHARMACIA & UPJOHN CO.
PA
XX
PI Bienkowski MJ, Gurney M;
XX
DR WPI: 2001-444208/48.
XX
PT Polypeptide comprising fragments of human aspartyl protease with
PT amyloid precursor protein processing activity and alpha-secretase
PT activity, for identifying modulators useful in treating Alzheimer's
PT disease -
XX
XX Example 12; Page 84; 187pp; English.
PS
XX The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
CC Aspl proteins which lack transmembrane domain or amino terminal
CC domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Aspl alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Aspl alpha-secretase activity, where modulators that increase
CC hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Aspl protease substrate is useful for assaying
CC hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Aspl proteolytic activity. The present sequence is wild-type
CC human amyloid precursor protein (APP) beta-secretase specific
CC substrate peptide, PHA-95812E. This peptide is used for assaying
CC the beta-secretase activity of human Aspartyl protease 2a (Asp2a)
CC

CC protein. The peptide is also used for determining the relationship
CC between Aspartyl protease 1 (Asp1) and APP protein.
XX
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10
| | | | | | | | | |
Db 1 SEVKMDAEFR 10

RESULT 4
AAE06899

ID AAE06899 standard; peptide; 10 AA.

AC AAE06899;

DT 23-OCT-2001 (first entry)

DE Human amyloid precursor protein wild-type beta-secretase peptide.

KW Human; aspartyl protease 2; Asp 2; beta-amyloid precursor protein; APP;
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; neurotrophic;
KW neuroprotective; antisense therapy; gene therapy.

OS Homo sapiens.

FX Key Location/Qualifiers

FT Cleavage-site 5..6

PN MO200150829-A2.

PD 19-JUL-2001.

PE 09-MAY-2001; 2001MO-IB00799.

PF 09-MAY-2001; 2001MO-IB00799.

PR 09-MAY-2001; 2001MO-IB00799.

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;

DR WPI; 2001-483072/52.

XX Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity

PS Claim 127; Page 80; 185pp; English.

XX The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta and
CC gamma-secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting

CC Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
CC blots. The present sequence is human amyloid precursor protein (APP)
CC wild type beta-secretase peptide used in beta-secretase assay.
XX
XX

SO Sequence 10 AA;

Query Match 100.0%; Score 49; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10
| | | | | | | | | |
Db 1 SEVKMDAEFR 10

RESULT 5
AAU06628

ID AAU06628 standard; Peptide; 10 AA.

AC AAU06628;

DT 24-OCT-2001 (first entry)

DE Asp2 recognition site from wild-type APP.

KW Aspartyl protease; Asp2; beta-secretase; neurotrophic;
KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW amyloid-beta; Abeta.

OS Homo sapiens.

FX Key Location/Qualifiers

FT Cleavage-site 5 /label= Asp2-protease_cleavage_site

PN MO200149098-A2.

PD 12-JUL-2001.

PE 09-MAY-2001; 2001MO-IB00798.

PF 09-MAY-2001; 2001MO-IB00798.

PR 09-MAY-2001; 2001MO-IB00798.

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;

DR WPI; 2001-502549/55.

XX Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity

PS Claim 127; Page 101; 185pp; English.

XX The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp2) protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp
CC proteins and vectors expressing them, and a polypeptide (isoform of
CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
CC APP or its fragment containing an APP cleavage site recognizable by a
CC mammalian beta-secretase, and further comprising two lysine residues at
CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
CC APP fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for

CC identifying inhibitors or modulators of human Asp2 activity and
 CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
 CC therapeutics for the treatment or prevention of Alzheimer's disease.
 CC APP comprising the APP-sw-beta-secretase peptide sequence (NLDA), which
 CC is associated with increased levels of Abeta processing is useful in
 CC assays relating the Alzheimer's research. The expression vector is useful
 CC for recombinantly expressing APP. Nucleic acids that hybridise to
 CC APP oligonucleotides are useful as probes or primers. The probes are
 CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence is a peptide substrate
 CC for Asp2 corresponding to the wild-type APP beta-secretase site.

XX Sequence 10 AA;

Query Match 100.0%; Score 49; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00042;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
 |||||||||
 Db 1 SEVKMDAEFR 10

RESULT 6
 AAU07227
 ID AAU07227 standard; Peptide; 10 AA.

AC AAU07227;

DT 24-OCT-2001 (first entry)

DE Human beta-amyloid protein precursor, APP-beta40 and 42 secretase site.

XX Human: aspartyl protease 1; Asp-1; nontropic; neuroprotective;
 KM aspartyl protease 2; Asp2; amyloid protein precursor; APP;
 KW beta-secretase; Alzheimer's disease; APP-beta40; APP-beta42.

XX Homo sapiens.

PN WO200149097-A2.

PD 12-JUL-2001.

PF 09-MAY-2001; 2001WO-IB00797.

PR 09-MAY-2001; 2001WO-IB00797.

XX (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;

XX WPI: 2001-502548/55.

PT Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity -

XX Claim 127; Page 101; 185pp; English.

CC The invention relates to a novel purified polypeptide comprising a
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
 CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. Also included is an isoform of amyloid protein precursor (APP)
 CC comprising the amino acid sequence of a APP or its fragment containing
 CC an APP cleavage site recognisable by a mammalian beta-secretase, and
 CC further comprising two lysine residues at the carboxyl terminus of the
 CC amino acid sequence of the mammalian APP or APP fragment. The

CC polypeptides are used for assaying for modulators of beta-secretase
 CC activity: identifying agents that inhibit the APP processing activity
 CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
 CC modulate the activity of Asp2; and for reducing cellular production of
 CC amyloid beta (Abeta) from APP. Agents identified by the above methods
 CC are useful for treating Alzheimer's disease; and for identifying
 CC modulators of amyloid-beta (Abeta) peptide production, for use in
 CC designing therapeutics for the treatment or prevention of Alzheimer's
 CC disease. Probes and primers derived from Asp nucleic acid sequences
 CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence represents the
 CC amino acid sequence of human amyloid protein precursor, APP-beta40
 CC and APP-beta42 secretase sites.

XX Sequence 10 AA;

Query Match 100.0%; Score 49; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00042;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
 |||||||||
 Db 1 SEVKMDAEFR 10

RESULT 7
 AAE02606
 ID AAE02606 standard; peptide; 10 AA.

AC AAE02606;

DT 10-AUG-2001 (first entry)

DE Human wild-type APP beta-secretase substrate peptide, PHA-95812E.

XX Human: alpha-secretase; amyloid precursor protein; APP; therapy;
 KW Alzheimer's disease; antialzheimer's; aspartyl protease 2a; Asp2a;
 KW beta-secretase.

XX Homo sapiens.

FT Key Location/Qualifiers

FT Cleavage-site 5..6

PN WO200123533-A2.

PD 05-APR-2001.

PF 22-SEP-2000; 2000WO-US26080.

PR 23-SEP-1999; 99US-0155493.

PR 23-SEP-1999; 99WO-US20881.

PR 13-OCT-1999; 99US-0416901.

PR 06-DEC-1999; 99US-0169232.

XX (PHAA) PHARMACIA & UPJOHN CO.

PI Gurney M, Bienkowski MJ;

XX WPI: 2001-290516/30.

PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
 PT protein, useful for the treatment of Alzheimer's disease -

XX Example 12; Page 85; 189pp; English.

CC The present invention relates to enzymes for cleaving the alpha-
 CC secretase site of the amyloid precursor protein (APP) and methods of
 CC identifying those enzymes. The methods may be used to identify enzymes
 CC that may be used to cleave the alpha-secretase cleavage site of the APP
 CC protein. The enzymes may be used to treat or modulate the progress of
 CC Alzheimer's disease. The present sequence is human wild-type amyloid
 CC precursor protein (APP) beta-secretase specific substrate peptide,

CC PHA-95812E. This peptide is used for assaying the beta-secretase activity
 CC of human Aspartyl protease 2a (Asp2a) protein. The peptide is also used
 CC for determining the relationship between Aspartyl protease 1 (Asp1) and
 CC APP protein.
 CC

SO Sequence 10 AA;

Query Match 100.0%; Score 49; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00042;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEFR 10
 |||||
 DB 1 SEVKMDAEFR 10

RESULT 8
 AAB6574
 ID AAB6574 standard; peptide; 10 AA.
 AC AAB6574;
 XX
 AC AAB6574;
 XX
 DT 12-APR-2001 (first entry)
 XX

DE Synthetic peptide derived from APP beta-secretase site.

KW Memapsin 2; neurotrophic; neuroprotective; amyloid precursor protein;
 KW APP; memapsin 2 inhibitor; Alzheimer's disease.

OS Synthetic.

XX WO200100665-A2.

XX 04-JAN-2001.

XX 27-JUN-2000; 2000WO-US17742.

XX 28-JUN-1999; 99US-0141363.

XX 30-NOV-1999; 99US-0168060.

XX 25-JAN-2000; 2000US-0177836.

XX 08-JUN-2000; 2000US-0178368.

XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX (UNIT) UNIT ILLINOIS FOUND.

XX Tang JUN, Hong L, Ghosh AK;

XX WPI: 2001-137933/14.

XX Novel memapsin 2 inhibitors which bind to active site of memapsin 2

XX having 2 catalytic aspartic residues and substrate binding cleft, used

XX to treat Alzheimer's disease by blocking amyloid precursor protein

XX cleavage -

XX Disclosure: Page 11; 86pp; English.

XX The present sequence is given in a specification relating to an inhibitor

XX of catalytically active memapsin 2. The inhibitor binds to the memapsin 2

XX active site, which is defined by the presence of two catalytic aspartic

XX residues and a substrate binding cleft. The inhibitor is useful for

XX the treatment and diagnosis of Alzheimer's disease. It is useful in

XX screens for individuals with a genetic predisposition to Alzheimer's

XX disease. The inhibitor is useful as a reagent for specifically binding to

XX memapsin 2 or memapsin 2 analogues and for aiding in memapsin 2

QY 1 SEVKMDAEFR 10
 |||||
 DB 1 SEVKMDAEFR 10

RESULT 9
 AAB46208
 ID AAB46208 standard; peptide; 10 AA.
 AC AAB46208;
 XX

QY 04-APR-2001 (first entry)

DE Human APP derived immunogenic peptide #4.

KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotrophic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.

OS Homo sapiens.

XX WO200072880-A2.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US14810.

XX 28-MAY-1999; 99US-0322289.

XX (NEUR-) NEURLAB LTD.

XX Schenk DB, Bard F, Vasquez NJ, Yednock T;

XX WPI: 2001-032104/04.

XX Preventing or treating a disease associated with amyloid deposits,

XX especially Alzheimer's disease, comprises administering amyloid

XX specific antibody -

XX Disclosure: Figure 19; 143pp; English.

XX This invention describes a novel method of preventing or treating a

XX disease associated with amyloid deposits of amyloid precursor protein

XX (APP) Abeta fragments in the brain of a patient, which comprises

XX administering to the patient: (a) an antibody that binds to Abeta, the

XX antibody binds to an amyloid deposit and induces a clearing response (Fc

XX receptor mediated phagocytosis) against it (b) a polypeptide containing

XX an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent

XX that induces an immunogenic response against residues 1-3 to 7-11 of

XX Abeta. The products of the invention have neurotrophic and neuroprotective

XX activity. The method is also useful for monitoring a course of treatment

XX being administered to a patient e.g. active and passive immunization. The

XX methods are useful for prophylactic and therapeutic treatment of

XX Alzheimer's disease.

XX Sequence 10 AA;

QY 1 SEVKMDAEFR 10
 |||||
 DB 1 SEVKMDAEFR 10

RESULT 10
 AAB61336
 ID AAB61336 standard; peptide; 10 AA.
 AC AAB61336;
 XX
 DT 02-APR-2001 (first entry)

XX Synthetic peptide from beta amyloid precursor protein.
 DE Memapsin 2; catalyst; Alzheimer's.
 XX
 OS Unidentified.
 XX
 PN WO200100663-A2.
 PD 04-JAN-2001.
 XX
 PF 27-JUN-2000; 2000WO-US17661.
 XX
 PR 28-JUN-1999; 99US-0141363.
 PR 30-NOV-1999; 99US-0168060.
 PR 25-JAN-2000; 2000US-0177836.
 PR 27-JAN-2000; 2000US-0178368.
 PR 08-JUN-2000; 2000US-0210292.
 XX
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 PI Tang JUN, Lin X, Koelsch G;
 DR WPI; 2001-102885/11.
 XX
 PT Purified recombinant catalytically active memapsin 2, used to screen
 PT inhibitors of it, which are used to treat and prevent Alzheimer's
 PT disease -
 XX
 PS Claim 6; Page 11; 86pp; English.
 CC The present invention relates to a purified recombinant
 CC catalytically active memapsin 2. The invention may be used for
 CC isolating inhibitors which are used to treat or prevent
 CC Alzheimer's disease. The invention may also be used to screen
 CC for individuals more genetically prone to develop Alzheimer's
 CC disease.
 CC
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 49; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00042;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SEVKMDAEFR 10
 | | | | | | | | | |
 DB 1 SEVKMDAEFR 10
 RESULT 11
 AAB75143
 ID AAB75143 standard; peptide; 11 AA.
 XX
 AC AAB75143;
 XX
 DT 08-AUG-2001 (first entry)
 XX
 DE APP beta-secretase cleavage site spanning peptide SEQ ID NO:1.
 XX
 KW Amyloid precursor protein; APP; Asp 1; endocrepisin 1; inhibition;
 KW transmembrane aspartyl proteinase; APP Swedish variant; neurotropic;
 KW neuroprotective; beta-secretase cleavage site; Alzheimer's disease;
 KW beta amyloid protein-related disease; antialzheimer.
 XX
 OS Homo sapiens.
 XX
 PN WO200131054-A1.
 PD 03-MAY-2001.
 XX
 PF 19-OCT-2000; 2000WO-GB04028.
 XX
 PR 22-OCT-1999; 99GB-0025136.

XX (SMIK) SMITHKLINE BEECHAM PLC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Christie G, Hussain I, Powell DJ;
 DR WPI; 2001-328654/34.
 XX
 PT Identifying inhibitors of Asp 1-mediated cleavage, for treating or
 PT preventing beta-amyloid protein-related disease, comprising measuring
 PT the extent of substrate cleavage in a reaction system containing Asp 1
 PT and a substrate -
 XX
 PS Disclosure; Page 3; 31pp; English.
 CC The present invention describes a method of screening for compounds
 CC which inhibit Asp 1-mediated cleavage of a polypeptide or protein
 CC substrate. The method comprises providing a reaction system comprising
 CC Asp 1 and substrate, and measuring the extent of cleavage of the
 CC substrate in the presence of test compound compared with that in the
 CC presence of the test compound. Also described are: (1) a method of
 CC screening for compounds which inhibit Asp 1 mediated cleavage of a
 CC polypeptide or protein substrate comprising providing a reaction system
 CC comprising Asp 1 and a labeled active site ligand, and measuring the
 CC extent of binding of the labeled ligand in the presence of test compound
 CC compared with that in the presence of the test compound; (2) a compound
 CC identified by the method; (3) a pharmaceutical composition comprising the
 CC compound of (2) and a carrier; (4) a method of inhibiting Asp 1 modulated
 CC amyloid precursor protein (APP) cleavage, or treating or prophylaxis of
 CC beta-amyloid protein-related disease, comprising administering to a
 CC patient a compound of (2); (5) a compound which is an inhibitor of Asp 1
 CC modulated APP cleavage; and (6) a method for treating or prophylaxis of
 CC beta-amyloid protein-related disease comprising administering a compound
 CC of (2) or (5). The compound which inhibits Asp 1 mediated cleavage of a
 CC polypeptide or protein is useful in therapy, in the preparation of a
 CC medicament for inhibiting Asp 1-modulated APP cleavage and for the
 CC treatment or prophylaxis of beta-amyloid protein-related disease.
 CC including Alzheimer's disease. The present sequence represents an APP
 CC beta-secretase cleavage site spanning peptide which can be used as a
 CC substrate in the method of the invention.
 CC
 SQ Sequence 11 AA;
 Query Match 100.0%; Score 49; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00046;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SEVKMDAEFR 10
 | | | | | | | | | |
 DB 2 SEVKMDAEFR 11
 RESULT 12
 AAB75144
 ID AAB75144 standard; peptide; 11 AA.
 XX
 AC AAB75144;
 XX
 DT 08-AUG-2001 (first entry)
 XX
 DE Asp 1 substrate sequence SEQ ID NO:3.
 XX
 KW Amyloid precursor protein; APP; Asp 1; endocrepisin 1; inhibition;
 KW transmembrane aspartyl proteinase; APP Swedish variant; neurotropic;
 KW neuroprotective; beta-secretase cleavage site; Alzheimer's disease;
 KW beta amyloid protein-related disease; antialzheimer.
 XX
 OS Homo sapiens.
 XX
 PN Key Location/Qualifiers
 FT Modified-site 1
 FT /note="N-terminally attached to maltose binding protein
 FT (MBP)"

XX WO200131054-A1.
PN
XX
XX 03-MAY-2001.
PD
XX
XX 19-OCT-2000; 2000WO-GB04028.
PF
XX
XX 22-OCT-1999; 99GB-0025136.
PR
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX
PI Christie G, Hussain I, Powell DJ;
DR WPI; 2001-328654/34.
XX
XX
PT Identifying inhibitors of Asp 1-mediated cleavage, for treating or
PT preventing beta-amyloid protein-related disease, comprises measuring
PT the extent of substrate cleavage in a reaction system containing Asp 1
PT and a substrate -
XX
XX
PS Disclosure; Page 3; 31pp; English.
XX
XX The present invention describes a method of screening for compounds
CC which inhibit Asp 1-mediated cleavage of a polypeptide or protein
CC substrate. The method comprises providing a reaction system comprising
CC Asp 1 and substrate, and measuring the extent of cleavage of the
CC substrate in the presence of test compound compared with that in the
CC presence of the test compound. Also described are: (1) a method of
CC screening for compounds which inhibit Asp 1 mediated cleavage of a
CC polypeptide or protein substrate comprising providing a reaction system
CC comprising Asp 1 and a labeled active site ligand, and measuring the
CC extent of binding of the labeled ligand in the presence of test compound
CC compared with that in the presence of the test compound; (2) a compound
CC identified by the method; (3) a pharmaceutical composition comprising the
CC compound of (2) and a carrier; (4) a method of inhibiting Asp 1 mediated
CC amyloid precursor protein (APP) cleavage, or treating or prophylaxis of
CC beta-amyloid protein-related disease, comprising administering to a
CC patient a compound of (2); (5) a compound which is an inhibitor of Asp 1
CC mediated APP cleavage; and (6) a method for treating or prophylaxis of
CC beta-amyloid protein-related disease comprising administering a compound
CC of (2) or (5). The compound which inhibits Asp 1 mediated cleavage of a
CC polypeptide or protein is useful in therapy, in the preparation of a
CC medicament for inhibiting Asp 1-mediated APP cleavage and for the
CC treatment or prophylaxis of beta-amyloid protein-related disease,
CC including Alzheimer's disease. The present sequence represents an Asp 1
CC substrate sequence which is given in the exemplification of the present
CC invention.
XX
XX Sequence 11 AA;
SQ
Query Match 100.0%; Score 49; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEVKMDAEFR 10
DB 2 SEVKMDAEFR 11
IIIIIIIIII
RESULT 13
ID AAB97468 standard; Protein; 11 AA.
XX
XX AAB97468;
AC
XX
XX 03-AUG-2001 (first entry)
DT
XX
XX Asp2 substrate wild-type beta-site peptide sequence.
DE
XX
XX Asp2; endocrepain 2; memapsin 2; beta-amyloid protein;
KW Alzheimer's disease; cortical lewy body disease; Parkinson's disease;
KW Asp2 inhibitor.

XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /Label= OTHER
FT /note= "optionally bound to maltose binding protein"
XX
XX WO200129563-A1.
XX
XX 26-APR-2001.
PD
XX
XX 19-OCT-2000; 2000WO-GB04039.
PF
XX
XX 21-OCT-1999; 99GB-0024957.
PR
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX
PI Christie G, Hussain I, Powell DJ;
DR WPI; 2001-300381/31.
XX
XX Screening for inhibitors of Asp 2 mediated polypeptide cleavage
PT comprises measuring substrate cleavage or ligand binding with a system
PT comprising Asp 2 and a substrate or labelled ligand in the presence or
PT absence of a test compound -
XX
XX
PS Disclosure; Page 3; 34pp; English.
XX
XX The present invention describes a method of screening for compounds which
CC inhibit Asp2 (also known as memapsin 2 and endocrepain 2) mediated
CC cleavage of a protein substrate, involving measuring the extent of
CC cleavage of the substrate in the presence and absence of the test
CC compound. Asp2 is thought to be involved in the cleavage of amyloid
CC precursor protein in which is excised to produce beta-amyloid. Beta-amyloid
CC is involved in the pathogenesis of Alzheimer's disease. Parkinson's
CC disease, cortical lewy body disease and vascular and cerebrovascular
CC diseases, and Asp2 inhibitors could be useful in their treatment. The
CC present sequence is an example of an Asp2 substrate.
XX
XX Sequence 11 AA;
SQ
Query Match 100.0%; Score 49; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEVKMDAEFR 10
DB 2 SEVKMDAEFR 11
IIIIIIIIII
RESULT 14
ID AAW70869 standard; peptide; 13 AA.
XX
XX AAW70869;
AC
XX
XX 04-FEB-1999 (first entry)
DT
XX
XX Beta-amyloid peptide to create a monoclonal antibody.
DE
XX
XX Beta-amyloid precursor protein; beta-APP; beta-amyloid peptide;
KW antibody; amyloid deposit; Alzheimer's disease.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX WO9844955-A1.
PN
XX
XX 15-OCT-1998.
PD
XX
XX 09-APR-1998; 98WO-US06900.
PF

```

XX 09-APR-1997; 97US-0041850.
PR (MCIN/) MCINIS P A.
PA (MIND-) MINDSET LTD.
XX
XX Chain DG;
XX
XX WPI: 1998-594476/50.
XX
XX Preventing or inhibiting progression of Alzheimer's Disease -
PT comprises use of recombinant DNA encoding an antibody specific for
PT the N- or C-terminus of an amyloid-beta peptide
XX
XX Example 1; Page 47; 58pp; English.
XX
XX The present sequence represents a peptide derived from beta-amyloid
CC precursor protein (beta-ApP). The peptide is a beta-amyloid
CC peptide and is used to produce a monoclonal antibody. The specification
CC describes a method for prevention or inhibition of progression of
CC Alzheimer's disease. The method comprises administering a composition
CC recombinant antibody end-specific for the N-terminus or the C-terminus
CC of an amyloid-beta peptide, operably linked to a promoter which is
CC expressed in the central nervous system. The recombinant antibody
CC molecules prevent the accumulation of beta-amyloid peptides in the
CC extracellular space, interstitial fluid and cerebrospinal fluid and the
CC aggregation of such peptides into amyloid deposits in the brain. They
CC also inhibit the progression of Alzheimer's disease by inhibiting the
CC interaction of beta-amyloid peptides mediating Alzheimer's disease
CC induced neurotoxicity and inhibiting the Alzheimer's disease induced
CC complement activation and cytokine release involved in the inflammatory
CC process.
XX
XX Sequence 13 AA:
SQ
XX
XX Query Match 100.0%; Score 49; DB 19; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 0.00056;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEVKMDAEPF 10
Db 3 SEVKMDAEPF 12
IIIIIIIII

RESULT 15
AAB06315
ID AAB06315 standard; peptide; 16 AA.
XX
XX AAB06315;
AC
XX
XX 03-OCT-2000 (first entry)
DT
XX
XX Human beta-amyloid precursor protein beta-secretase cleavage site.
DE
XX
XX Human: beta-amyloid precursor protein; beta-ApP; beta-secretase;
XX subtilisin-kexin isoenzyme 1; SKI-1;
XX pro-brain-derived neurotrophic factor; PROBDNF; antidiabetic;
XX cytostatic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia;
XX liver steatosis; Ras-dependent cancer; restenosis;
XX amyloid protein formation.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX Cleavage-site 8..9
XX
XX WO200026348-A2.
XX
XX 11-MAY-2000.
XX
XX 04-NOV-1999; 99WO-CA01058.
XX

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PR 04-NOV-1998; 98CA-2249648.
XX
XX (RECL-) INST RECH CLINIQUES MONTREAL.
PA
XX
XX Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;
XX
XX WPI: 2000-365601/31.
XX
XX Novel soluble proteic fragment of subtilisin-kexin isoenzyme for
PT producing a polypeptide useful for treating hypercholesterolemia, liver
PT steatosis and amyloidosis, comprises a specific amino acid sequence -
XX
XX Example 4; Page 51; 119pp; English.
XX
XX The present sequence is the beta-secretase site of human beta-amyloid
CC precursor protein (beta-ApP). The sequence may be cleaved
CC by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1
CC (SKI-1), a type-I membrane-bound protease. Peptides which bind to and
CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for
CC screening inhibitors of SKI-1 activity, or for screening enhancers of
CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1
CC catalytic site may be used as inhibitors of SKI-1 activity. They may be
CC used to treat diseases involving overexpression of SKI-1 or SKI-1
CC substrate. Such diseases include hypercholesterolemia, high levels of
CC fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,
CC Ras-dependent cancer, restenosis and amyloid protein formation.
XX
XX Sequence 16 AA:
SQ
XX
XX Query Match 100.0%; Score 49; DB 21; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 0.00071;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEVKMDAEPF 10
Db 4 SEVKMDAEPF 13
IIIIIIIII

Search completed: October 29, 2002, 10:26:43
Job time : 23.1429 secs

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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:36 ; Search time 10.4286 seconds
(without alignments)
92.140 Million cell updates/sec

Title: US-09-580-018-4

Perfect score: 49

Sequence: 1 SEVKMDAEFR 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	49	100.0	57	2	E60045	Alzheimer's disease
2	49	100.0	57	2	F60045	Alzheimer's disease
3	49	100.0	57	2	G60045	Alzheimer's disease
4	49	100.0	57	2	D60045	Alzheimer's disease
5	49	100.0	57	2	A60045	Alzheimer's disease
6	49	100.0	57	2	B60045	Alzheimer's disease
7	49	100.0	82	2	P00438	Alzheimer's disease
8	49	100.0	695	1	A49795	Alzheimer's disease
9	49	100.0	770	1	Q8H0U4	Alzheimer's disease
10	44	89.8	33	2	S23094	beta-amyloid protein
11	44	89.8	695	2	A27485	Alzheimer's disease
12	44	89.8	695	2	S00550	Alzheimer's disease
13	43	87.8	747	2	JH0773	Alzheimer's disease
14	39	79.6	142	2	E89026	Protein F13A2.1 [I
15	35	71.4	774	2	AG1565	autolysin (amidase
16	34	69.4	626	2	AF0358	conserved hypochet
17	34	3562	2	A47171	chondroitin sulfat	
18	34	69.4	4563	1	LPHUB	apolipoprotein B-1
19	33	67.3	927	2	T38127	phosphoprotein - F
20	33	67.3	1245	2	G86404	probable P-glycop
21	32	65.3	263	2	D84226	hypothetical prote
22	32	65.3	354	2	S51143	FMO-protein - Chlo
23	32	65.3	392	2	T49471	mucin (muc3) relat
24	32	65.3	426	2	G75187	probable trehalose
25	32	65.3	625	2	D86244	protein Ser/Thr pr
26	32	65.3	700	2	E84131	transcription anti
27	32	65.3	929	2	T52517	hypothetical prote
28	32	65.3	1044	2	H97186	glycosyltransferas
29	32	65.3	1265	2	T51498	hypothetical prote

ALIGNMENTS

30	32	65.3	1906	2	AD2443	hypothetical prote
31	32	65.3	2514	2	T37320	ataxia telangiecta
32	32	65.3	2619	2	T24588	hypothetical prote
33	31	63.3	87	2	A97842	hypothetical prote
34	31	63.3	155	2	F75040	hypothetical prote
35	31	63.3	178	2	C64168	hypothetical prote
36	31	63.3	182	2	AC0449	conserved hypochet
37	31	63.3	183	2	S56460	probable alpha hel
38	31	63.3	183	2	C91280	probable alpha hel
39	31	63.3	183	2	C86121	conserved alpha hel
40	31	63.3	183	2	AD1056	conserved hypochet
41	31	63.3	198	2	S48290	OX40 ligand - mus
42	31	63.3	199	2	F72060	conserved hypochet
43	31	63.3	199	2	C86564	CT471 hypothetical
44	31	63.3	226	2	G69129	hypothetical prote
45	31	63.3	279	2	T41124	single-stranded DN

RESULT 1

E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C:Species: Ovis sp. (sheep)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: E60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56130
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match
Best Local Similarity 100.0%; Score 49; DB 2; Length 57;
Pred. No. 0.0017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEFR 10
DB 1 SEVKMDAEFR 10

RESULT 2

F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: F60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56127; NID:91895; PIDN:CAA39592.1; PID:91896
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match
Best Local Similarity 100.0%; Score 49; DB 2; Length 57;
Pred. No. 0.0017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEFR 10
DB 1 SEVKMDAEFR 10

```

RESULT 3
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      100.0%; Score 49; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAER 10
DB 1 SEVKMDAER 10

RESULT 4
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: D60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56124
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      100.0%; Score 49; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAER 10
DB 1 SEVKMDAER 10

RESULT 5
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      100.0%; Score 49; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 SEVKMDAER 10
DB 1 SEVKMDAER 10

RESULT 6
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56128; NID:92165; PIDN:CA9593.1; PID:92166
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      100.0%; Score 49; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAER 10
DB 1 SEVKMDAER 10

RESULT 7
P00438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: P00438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 186, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
A:Reference number: P00438; MUID:93075180
A:Accession: P00438
A:Molecule type: DNA
A:Residues: 1-82 <DAY>
A:Cross-references: GB:M83558; GB:M83657
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match      100.0%; Score 49; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAER 10
DB 12 SEVKMDAER 21

RESULT 8
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991

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A>Title: Homology of the amyloid beta protein precursor in monkey and human supports a p
 A:Reference number: A49795; MUID:91273117
 A:Accession: A49795
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-695 <POD>
 A:Cross-references: GB:M58727; NID:9342062; PIDN:AAA36829.1; PID:9342063
 A:Cross-references: GB:M58727; NID:9342062; PIDN:AAA36829.1; PID:9342063
 C:Keywords: Alzheimer's disease amyloid beta protein; animal knnltz-type proteinase 1
 C:Keywords: alternative splicing

Query Match 100.0%; Score 49; DB 1; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKDAEFR 10
 DB 592 SEVKDAEFR 601

RESULT 9

ORHUA4

Alzheimer's disease amyloid beta protein precursor [validated] - human
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibi
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
 protein precursor splice form APP(770)
 C:Species: Homo sapiens (man)

C>Date: 30-Jun-1987 #sequence revision 28-Jul-1995 #text change 15-Sep-2000

C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44
 4688; A28583; A29302; A60809; J00038; S06121; A60311; A38344; S23076; S38252; S3
 R:Lemaitre, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
 Nucleic Acids Res. 17, 517-522, 1989

A>Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
 A:Reference number: S02260; MUID:89128427

A:Accession: S02260
 A:Molecule type: DNA

A:Residues: 1-288, 'V', 365-770 <LEM1>

A:Cross-references: EMBL:X13466

A>Note: alternative splice form APP(695)

R:Lemaitre, H.G.
 submitted to the EMBL Data Library, November 1988

A:Reference number: S05194
 A:Accession: S05194

A:Molecule type: DNA

A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>

A:Cross-references: EMBL:X13466; NID:935598; PIDN:CAA1830.1; PID:9871360

A>Note: alternative splice form APP(695)

R:La Pauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A>Title: Characterization of the 5'-end region and the first two exons of the beta-prote
 A:Reference number: A32277; MUID:89165870

A:Accession: A32277
 A:Molecule type: DNA

A:Residues: 1-75 <LAR>

A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AA013654.1; PID:9516074

R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989

A>Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
 A:Reference number: A33260; MUID:89392030

A:Accession: A33260
 A:Molecule type: DNA

A:Residues: 656-737 <LOH>

A:Cross-references: GB:M29270; NID:9178863; PIDN:AAA51768.1; PID:9178865

R:Pirelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990

A>Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
 A:Reference number: A35486; MUID:90321244

A:Accession: A35486
 A:Molecule type: DNA

A:Residues: 672-710 <PRE1>

A>Note: 693-Gln was found in DNA isolated from HCMVA-D patients
 R:Yoshihaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 87, 257-263, 1990

A>Title: Genomic organization of the human amyloid beta-protein precursor gene.

A:Reference number: I39451; MUID:90236318

A:Accession: I39452

A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/
 A:Molecule type: DNA

A:Residues: 1-770 <YOS1>

A:Cross-references: GB:M33112; NID:9178613; PIDN:AA59502.1; PID:9178616

A:Accession: I39451

A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/
 A:Molecule type: DNA

A:Residues: 1-530, 'QWIMPIYPAFWKAYGR' <YOS2>

A:Cross-references: GB:M34875; NID:9178608; PIDN:AA59501.1; PID:9178615

R:Yoshihaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 102, 291-292, 1991

A:Reference number: A59020; MUID:91340168

A:Accession: A59020

A:Contents: annotation; erratum

A>Note: revised physical map for reference I39451

R:Levy, E.; Garman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du
 Science 248, 1124-1126, 1990

A>Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo
 A:Reference number: I39453; MUID:90260663

A:Accession: I39453

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 656-737 <LEVY>

A:Cross-references: GB:M37896; NID:9178618; PIDN:AAA51727.1; PID:9178620

A>Note: a mutation with 693-Gln is presented

R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991

A>Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe
 A:Reference number: I59562; MUID:92022553

A:Accession: I59562

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 688-716, 'F', 718-737 <MUR>

A:Cross-references: GB:S57655; NID:9236720; PIDN:AA819991.1; PID:9236721

R:Kamano, K.; Orr, H.T.; Payami, H.; Wilsman, E.M.; Alonso, M.E.; Puls, S.M.; Anders
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Mart
 Am. J. Hum. Genet. 51, 998-1014, 1992

A>Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t
 A:Reference number: A44017; MUID:93035397

A:Accession: A44017

A:Molecule type: DNA

A:Residues: 687-692, 'G', 694-718 <RAM1>

A:Cross-references: GB:S45135; NID:9257377; PIDN:AA823645.1; PID:9257378

A:Experimental source: Familial Alzheimer disease family SB

A>Note: sequence extracted from NCBI backbone (NCBI:115374)

A:Accession: B44017

A:Molecule type: DNA

A:Residues: 687-718 <RAM2>

A:Cross-references: GB:S45136; NID:9257379; PIDN:AA823646.1; PID:9257380

A:Experimental source: Familial Alzheimer disease family LIT

A>Note: this sequence has a silent mutation

R:Kang, J.; Lemaitre, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.
 Nature 335, 733-736, 1987

A>Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-sur
 A:Reference number: A03134; MUID:87144572

A:Accession: A03134

A:Molecule type: mRNA

A:Residues: 1-288, 'V', 365-770 <KAN>

A:Cross-references: GB:Y00264; NID:928525; PIDN:CAA68374.1; PID:928526

A>Note: alternative splice form APP(695)

R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.;
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987

A>Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascula
 A:Reference number: A29030; MUID:87231971

A:Accession: A29030

A:Molecule type: mRNA

A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>

A:Cross-references: GB:M6765; NID:9178539; PIDN:AAA51722.1; PID:9178540

A>Note: the authors translated the codon GAG for residue 647 as Asp

R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987

A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
 A:Reference number: A47584; MUID:87120328
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756, 'S', '758-770 <GOL>
 A:Cross-references: GB:M15533; NID:q178706; PIDN:AAA5540.1; PID:q178707
 A:Note: Experimental source: brain
 R:Tanzil, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
 Science 235, 880-884, 1987
 A:Title: Amyloid beta protein gene: CDNA, mRNA distribution, and genetic linkage near th
 A:Reference number: A47585; MUID:87120329
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TANI>
 A:Cross-references: GB:M15532; NID:q177957; PIDN:AAA51564.1; PID:q177958
 R:Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mueller
 EMBO J. 7, 949-957, 1988
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
 A:Reference number: 502638; MUID:88296437
 A:Accession: 502638
 A:Molecule type: mRNA
 A:Residues: 672-678 <DYR>
 R:Tanzil, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
 Nature 331, 528-530, 1988
 A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
 A:Reference number: 500707; MUID:88122640
 A:Accession: 500707
 A:Molecule type: mRNA
 A:Residues: 286-344, 'I', '365-366 <TAN2>
 A:Cross-references: EMBL:X06982; NID:q28817; PIDN:CAA30042.1; PID:q929612
 A:Note: Experimental source: promyelocytic leukemia cell line HL60
 R:Porte, P.; Gonzalez-Demhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
 Nature 331, 523-527, 1988
 A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
 A:Reference number: 500925; MUID:88122639
 A:Accession: 500925
 A:Molecule type: mRNA
 A:Residues: 1-344, 'I', '365-770 <PRO2>
 A:Cross-references: GB:X06989; EMBL:Y00297; NID:q28720; PIDN:CAA30050.1; PID:q28721
 A:Note: Alternative splice form APP(751)
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
 A:Reference number: A38949; MUID:88122641
 A:Accession: A38949
 A:Molecule type: mRNA
 A:Residues: 287-367 <KIT>
 A:Cross-references: GB:X06981; NID:q28816; PIDN:CAA30041.1; PID:q929611
 A:Note: Experimental source: glioblastoma cell line
 A:Note: alternative splice form APP(770)
 R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three F
 A:Reference number: A30320
 A:Accession: A30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', '365-770 <VIT1>
 A:Accession: B30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 122-288, 'V', '365-770 <VIT2>
 A:Accession: C30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 606-770 <VIT3>
 R:Zaini, S.B.; Sallim, M.; Chou, W.G.; Sajdel-Sulowska, E.M.; Majocha, R.E.; Marotta, C.A
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
 A:Reference number: A31087; MUID:88124954
 A:Accession: A31087
 A:Molecule type: mRNA

A:Residues: 507-770 <ZAI>
 A:Cross-references: GB:M18734; NID:q178572; PIDN:AAA51726.1; PID:q178573
 A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue
 8 as Val, GAG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue
 A:Note: the cited Genbank accession number, J03594, is not in release 101.0
 R:Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther,
 Query Match 100.0%; Score 49; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 SEVKMDAEFR 10
 |||||
 Db 667 SEVKMDAEFR 676
 RESULT 10
 S23094
 beta-amyloid protein precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
 C:Accession: S23094
 R:Kojima, S.; Omori, M.
 FEBS Lett. 304, 57-60, 1992
 A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic protein
 A:Reference number: S23094; MUID:92316198
 A:Accession: S23094
 A:Molecule type: protein
 A:Residues: 1-33 <KOJ>
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinases
 Query Match 89.8%; Score 44; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 SEVKMDAEF 9
 |||||
 Db 1 SEVKMDAEF 9
 RESULT 11
 A27485
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
 N:Alternate names: proteinase nexin II
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
 C:Accession: A27485; S19727; I49485
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein pr
 A:Reference number: A27485; MUID:88106489
 A:Accession: A27485
 A:Molecule type: mRNA
 A:Residues: 1-695 <YAM>
 A:Cross-references: GB:M18373; NID:q191568; PIDN:AAA37139.1; PID:q309085
 A:Experimental source: brain
 R:de Strooper, B.; van Leuven, F.; van den Berghe, H.
 Biochim. Biophys. Acta 1129, 141-143, 1991
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is clos
 A:Reference number: S19727; MUID:92096458
 A:Accession: S19727
 A:Molecule type: mRNA
 A:Residues: 1-210, 'G', '212-220, 'S', '222-396, 'A', '398-402, 'T', '404-448, 'A', '450-695 <STR>
 A:Cross-references: EMBL:X59379
 R:Izumi, R.; Yamada, T.; Yoshikali, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
 Gene 112, 189-195, 1992
 A:Title: Positive and negative regulatory elements for the expression of the Alzhelme
 A:Reference number: I49485; MUID:92209998
 A:Accession: I49485
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-19 <RES>
 A:Cross-references: GB:D10603; NID:q220328; PIDN:BA01456.1; PID:q220329

C:Genetics:
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase A
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 89.8%; Score 44; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEF 9
|||||
Db 592 SEVKMDAEF 600

RESULT 12

S00550 Alzheimer's disease amyloid beta protein precursor - rat

N:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999

C:Accession: S00550; A41245; A39820; S46251
R:Shivers, B.D.; Hilblch, C.; Muthaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988

A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A:Reference number: S00550; MUID:88312583
A:Accession: S00550

A:Molecule type: mRNA

A:Residues: 1-695 <SH1>
A:Cross-references: EMBL:X07648; NID:955616; PIDN:CA430488.1; PID:955617

R:Schubert, D.; Schroeder, R.; Lacorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988

A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A:Reference number: A41245; MUID:88264430
A:Accession: A41245

A:Molecule type: protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A:Note: evidence for heparan sulfate attachment

R:Hesse, L.; Behner, D.; Masters, C.L.; Muthaup, G.
FEBS Lett. 349, 109-116, 1994

A:Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MUID:94320627
A:Accession: S46251

A:Contents: annotation: copper binding sites
A:Note: rat peptides were isolated but not sequenced

R:Potempska, A.; Styles, J.; Mehra, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991

A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A:Reference number: A39820; MUID:91217087
A:Accession: A39820

A:Status: preliminary
A:Molecule type: protein

A:Residues: 18-32 <POT>

A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase A

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase A
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-648/Domain: transmembrane #status predicted <TM>

Query Match 89.8%; Score 44; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEF 9
|||||
Db 592 SEVKMDAEF 600

RESULT 13
JH0773 Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773
R:Okado, H.; Okamoto, H.

Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: development
A:Reference number: JH0773; MUID:93129227
A:Accession: JH0773

A:Molecule type: mRNA

A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151

A:Experimental source: larva

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteins
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 87.8%; Score 43; DB 2; Length 747;
Best Local Similarity 80.0%; Pred. No. 0.58;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEF 10
|||||
Db 644 SEVKMDSEYR 653

RESULT 14

E89026 protein F13A2.1 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: E89026

R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C-
elegans/

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A:Accession: E89026

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-142 <STO>

A:Cross-references: GB:chr_V; PIDN:AAB69895.1; PID:g2384795; GSPDB:GN00023; CESP:F13A
C:Genetics:

A:Gene: F13A2.1

A:Map position: 5

Query Match 79.6%; Score 39; DB 2; Length 142;
Best Local Similarity 77.8%; Pred. No. 0.66;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 EVKMDAEFR 10
|||
Db 56 EVKMDAEFR 64

RESULT 15

AG1565 autolysin (amidase) homolog lin1064 [imported] - Listeria innocua (strain C1p11262)

C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AG1565

R:Dominguez-Bernal, C.; Duchaud, E.; Durand, L.; Dussureget, O.; Entian, K.D.; Fsihi,
D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maltournam, A.;
Ok, C.; Schlutner, T.; Simoes, N.; Tjereez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla

A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1565

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-774 <GLA>

A:Cross-references: GB:AL592022; PIDN:CAC96295.1; PID:g16413523; GSPDB:GN00178
A:Experimental source: strain C1p11262

C:Genetics:

A:Gene: lin1064

Query Match 71.4%; Score 35; DB 2; Length 774;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 VKMDAEFR 10
: : : : :
Db 123 IKIDAEFR 130
Search completed: October 29, 2002, 10:31:01
Job time : 11.4286 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:36 ; Search time 5 Seconds

(without alignments)
77.439 Million cell updates/sec

Title: US-09-580-018-4
Perfect score: 49
Sequence: 1 SEVKMDAER 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	57	1 A4_PIG	Q29023 sus scrofa
2	49	100.0	57	1 A4_URSM	Q29149 ursus marit
3	49	100.0	58	1 A4_CANRA	Q28280 canis famill
4	49	100.0	58	1 A4_RABIT	Q28748 oryctolagus
5	49	100.0	58	1 A4_SHEEP	Q28757 ovis aries
6	49	100.0	59	1 A4_BOVIN	Q28053 bos taurus
7	49	100.0	751	1 A4_SALISC	Q95241 salmistr sci
8	49	100.0	770	1 A4_HUMAN	P05067 homo sapien
9	44	89.8	770	1 A4_MOUSE	P12023 mus musculu
10	44	89.8	770	1 A4_RAT	P08592 rattus norv
11	37	75.5	269	1 T2S1_STRFT	O52512 streptomyc
12	34	69.4	3562	1 PGCV_CHICK	O90513 gallus gall
13	34	69.4	4563	1 APB_HUMAN	P04114 homo sapien
14	33	67.3	927	1 CC15_SCHPO	Q09822 schizosacch
15	32	65.3	263	1 Y6B3_HALNI	Q9hr12 halobacteri
16	32	65.3	354	1 BCPA_CHLIT	Q46135 chlorobium
17	32	65.3	365	1 BCPA_CHITE	Q46393 chlorobium
18	31	63.3	178	1 YUGA_HAEIN	P45076 haemophilus
19	31	63.3	183	1 YUGA_ECOLI	P26550 escherichia
20	31	63.3	198	1 TNF4_MOUSE	P43488 mus musculu
21	31	63.3	279	1 RFA2_SCHPO	O92373 schizosacch
22	31	63.3	479	1 Y098_MYCPN	P55535 mycoplasma
23	31	63.3	1024	1 Y075_MYCGE	P47321 mycoplasma
24	30	61.2	78	1 RL31_RICCN	O921d0 rickettsia
25	30	61.2	78	1 RL31_RICPR	O92427 rickettsia
26	30	61.2	197	1 OM26_HAEIN	O57483 haemophilus
27	30	61.2	356	1 RFL_BACSU	P45872 bacillus su
28	30	61.2	394	1 EFTU_BOCAL	O31297 buchnera ap
29	30	61.2	400	1 YF74_ARCFU	O28598 archaeoglob
30	30	61.2	419	1 P47K_PSECL	P31221 pseudomonas
31	30	61.2	463	1 YD14_SCHPO	O92342 schizosacch
32	30	61.2	464	1 SPN5_SCHPO	P48010 schizosacch
33	30	61.2	656	1 V091_FOMPV	O72896 fowlpox vitr

34	30	61.2	666	1 ZP2_RABIT	P48829 oryctolagus
35	30	61.2	745	1 ZP2_HUMAN	Q05996 homo sapien
36	30	61.2	745	1 ZP2_MACRA	O77726 macaca radi
37	30	61.2	766	1 METE_YEAST	P05694 saccharomyc
38	30	61.2	827	1 YAIL_RHISN	P55552 rhizobium s
39	30	61.2	926	1 UVRA_AQUAE	O66911 aquifex aeo
40	30	61.2	1391	1 YLD5_CAEEL	Q03570 caenorhabdi
41	30	61.2	1514	1 NX1A_RAT	Q63372 rattus norv
42	30	61.2	4639	1 DYHC_DROME	P37276 drosophila
43	29	59.2	185	1 RRF_ECOLI	P16174 escherichia
44	29	59.2	221	1 GSPJ_VIBCH	P45776 vibrio chol
45	29	59.2	274	1 YA99_SCHPO	Q09787 schizosacch

ALIGNMENTS

RESULT 1	ID	AA_PIG	STANDARD:	PRT:	57 AA.
AC	Q29023	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid				
DE	protein (Beta-APP) (A-beta)] (Fragment).				
GN	APP				
OS	Sus scrofa (Pig).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OX	NCBI_TaxID=9823;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=92017079; PubMed=1656157;				
RA	Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;				
RT	"Conservation of the sequence of the Alzheimer's disease amyloid				
RT	peptide in dog, polar bear and five other mammals by cross-species				
RT	polymerase chain reaction analysis."				
RL	Brain Res. Mol. Brain Res. 10:299-305(1991).				
CC	-1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO				
CC	INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN				
CC	G10) (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-1- SIMILARITY: BELONGS TO THE APP FAMILY.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	-----				
DR	EMBL: X56127; CAA39592.1; -				
DR	HSSP: P05067; 1BA4.				
DR	InterPro: IPR001868; A4_APP.				
DR	PROSITE: PS00319; A4_EXTRA; PARTIAL.				
DR	PROSITE: PS00320; A4_INTRA; PARTIAL.				
KW	Glycoprotein; Amyloid; Neurone; Transmembrane.				
FT	NON_TER	1			
FT	CHAIN	6			
FT	DOMAIN	<1			
FT	TRANSMEM	34			
FT	NON_TER	57			
FT	SEQUENCE	57 AA: 6172 MW: 84209888BA82DFA CRC64;			
SO	Query Match	100.0%; Score 49; DB 1; Length 57;			
QY	Best Local Similarity	100.0%; Pred. No. 0.0014;			
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
	1 SEVKMDAER 10				

```

Db      1 SEVKMDAEPF 10

RESULT 2
ID      A4_URSWA      STANDARD:      PRT:      57 AA.
AC      029149;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-ApP) (A-beta)] (Fragment).
GN      APP.
OS      Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC      Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX      NCBI_TaxID=9615;

[1]
RN      SEQUENCE FROM N.A.
RP      TISSUE=Brain;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC      or send an email to license@isb-sib.ch).
-----
CC      EMBL; X56128; CAA39593.1; -.
CC      HSSP; P05067; 1AM4.
CC      InterPro; IPR001868; A4_APP.
CC      PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC      PROSITE; PS00320; A4_INTRA; PARTIAL.
CC      Glycoprotein; Amyloid; Neurone; Transmembrane.
CC      NON_TER      1
CC      CHAIN      6 48      BETA-AMYLOID PROTEIN (POTENTIAL).
CC      DOMAIN      <1 33      EXTRACELLULAR (POTENTIAL).
CC      TRANSMEM      34 57      POTENTIAL.
CC      NON_TER      57
CC      SEQUENCE      57 AA: 6172 MW: 84209D88BA82DFA CRC64;

Query Match      100.0%; Score 49; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 SEVKMDAEPF 10
Db      1 SEVKMDAEPF 10

RESULT 3
ID      A4_CANFA      STANDARD:      PRT:      58 AA.
AC      028280;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-ApP) (A-beta)] (Fragment).
GN      APP.
OS      Canis familiaris (Dog).

```

```

CC      Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
CC      Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX      NCBI_TaxID=9615;

[1]
RN      SEQUENCE FROM N.A.
RP      TISSUE=Kidney;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
-----
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CC      or send an email to license@isb-sib.ch).
-----
CC      EMBL; X56125; CAA39590.1; -.
CC      HSSP; P05067; 1BA4.
CC      InterPro; IPR001868; A4_APP.
CC      PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC      PROSITE; PS00320; A4_INTRA; PARTIAL.
CC      Glycoprotein; Amyloid; Neurone; Transmembrane.
CC      NON_TER      1
CC      CHAIN      7 49      BETA-AMYLOID PROTEIN (POTENTIAL).
CC      DOMAIN      <1 34      EXTRACELLULAR (POTENTIAL).
CC      TRANSMEM      35 58      POTENTIAL.
CC      NON_TER      58
CC      SEQUENCE      58 AA: 6285 MW: 8469D488A2E12DFA CRC64;

Query Match      100.0%; Score 49; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 SEVKMDAEPF 10
Db      2 SEVKMDAEPF 11

RESULT 4
ID      A4_RABIT      STANDARD:      PRT:      58 AA.
AC      028748;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-ApP) (A-beta)] (Fragment).
GN      APP.
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxID=9986;

[1]
RN      SEQUENCE FROM N.A.
RP      TISSUE=Brain;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

```

```
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: X56129; CAA39594.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KM Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; FA34209D8EBA82D CRC64;

Query Match 100.0%; Score 49; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEFR 10
   |||||||
Db 1 SEVKMDAEFR 10

RESULT 5
A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
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DR EMBL: X56130; CAA39595.1; -.
DR HSSP: P05067; 1AML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KM Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; FA34209D8EBA82D CRC64;

Query Match 100.0%; Score 49; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEFR 10
   |||||||
Db 1 SEVKMDAEFR 10

RESULT 6
A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56124; CAA39589.1; -.
DR EMBL: X56126; CAA39591.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KM Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 35 58 POTENTIAL.
FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
FT
```

FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;
Query Match 100.0%; Score 49; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10
| | | | | | | | | |
Db 2 SEVKMDAEFR 11

RESULT 7
A4_SAIISC STANDARD; PRT; 751 AA.
ID A4_SAIISC
AC C95241;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor [contains: Beta-amyloid protein (Beta-ApP) (A-beta)].
GN APP.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy E., Amorim A., Frandone B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy".
RL Neurobiol. Aging 16:805-808(1995).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NKX1 MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC
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CC
CC EMBL; S81024; AAD14347.1; -
DR HSP; P05067; IAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA.
DR PRINTS; PR00759; BASICTPASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurope; Transmembrane; Alternative splicing;
KW Signal; Serine protease inhibitor.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 751 A4 PROTEIN.
FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).
FT

FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 681 704 POTENTIAL.
FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
FT ACT_SITE 301 302 REACTIVE BOND.
FT DISULFID 291 341 BY SIMILARITY.
FT DISULFID 300 324 BY SIMILARITY.
FT DISULFID 316 337 BY SIMILARITY.
FT CARBOHYD 523 523 N-LINKED (GLCNAC...) (PROBABLE).
FT CARBOHYD 552 552 N-LINKED (GLCNAC...) (PROBABLE).
SQ SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;
Query Match 100.0%; Score 49; DB 1; Length 751;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10
| | | | | | | | | |
Db 648 SEVKMDAEFR 657

RESULT 8
A4_HUMAN STANDARD; PRT; 770 AA.
ID A4_HUMAN
AC P05067; P09000; Q16011;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II) (PN-II) (APPI) [contains: Beta-amyloid protein (beta-ApP) (A-beta)].
GN APP OR A4 OR CVAP OR AD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor".
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine protease inhibitors".
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PrEA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons".
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M., Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for sequencing of a 300 kb region of human APP locus".
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [5]
RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;
RX

RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 RN [6]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity.";
 RL Nature 331:530-532(1988).
 RN [17]
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
 RX MEDLINE=87231971; PubMed=3035574;
 RA Roakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [8]
 RP SEQUENCE OF 507-770 FROM N.A.
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [9]
 RP SEQUENCE OF 672-681.
 RX MEDLINE=88035004; PubMed=3312495;
 RA Padridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tourtelotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels.";
 RL J. Neurochem. 49:1394-1401(1987).
 RN [10]
 RP SEQUENCE OF 739-770 FROM N.A.
 RX MEDLINE=90236318; PubMed=2110105;
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";
 RL Gene 87:257-263(1990).
 RN [11]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [12]
 RP SEQUENCE OF 18-50.
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [13]
 RP IDENTITY OF APP WITH NEXIN-II.
 RA MEDLINE=89384866; PubMed=2506449;
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
 RA Sinha S.;
 RT "The secreted form of the Alzheimer's amyloid precursor protein with
 RT the Kunitz domain is protease nexin-II.";
 RL Nature 341:144-147(1989).
 RN [14]
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RX MEDLINE=90211252; PubMed=1969731;
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
 RT disease amyloid protein precursor.";

RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
 RN [15]
 RP COMPLEX WITH G(O).
 RX MEDLINE=93186965; PubMed=8446172;
 RA Nishimoto I., Okamoto T., Matsura Y., Takahashi S., Okamoto T.,
 RA Murayama Y., Ogata E.;
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 RT protein G(O).";
 RL Nature 362:75-79(1993).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
 RX MEDLINE=99215582; PubMed=10201399;
 RA Rossjohn J., Cappai R., Fell S.C., Henry A., McIntyre W.J.,
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RT "Crystal structure of the N-terminal, growth factor-like domain of
 RT Alzheimer amyloid precursor protein.";
 RL Nat. Struct. Biol. 6:327-331(1999).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
 RX MEDLINE=91104913; PubMed=2125487;
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kosiakof A.A.;
 RT "X-ray crystal structure of the protease inhibitor domain of
 RT Alzheimer's amyloid beta-protein precursor.";
 RL Biochemistry 29:10018-10022(1990).
 RN [18]
 RP STRUCTURE BY NMR OF 289-344.
 RX MEDLINE=92031488; PubMed=1718421;
 RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,
 RA Kamark M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
 RA Tamburlini P.P.;
 RT "Sequential NMR resonance assignment and structure determination of
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
 RT precursor protein.";
 RL Biochemistry 30:10467-10478(1991).
 RN [19]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=94281210; PubMed=7516706;
 RA Talafous J., Marchowski K.J., Kiopman G., Zagorski M.G.;
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
 RL Biochemistry 33:7788-7796(1994).
 RN [20]
 RP STRUCTURE BY NMR OF 696-706.
 RX MEDLINE=97128622; PubMed=8973180;
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
 RT membrane-mimicking environment.";
 RL Biochemistry 35:16094-16104(1996).
 RN [21]
 RP STRUCTURE BY NMR OF 672-711.
 RX MEDLINE=98359783; PubMed=9693002;
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscible
 RT environment. Is the membrane-spanning domain where we think it is?";
 RL Biochemistry 37:11064-11077(1998).
 RN [22]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=20400066; PubMed=10940222;
 RA Poulsen S.A., Watson A.A., Craik D.J.;
 RT "Solution structures in aqueous SDS micelles of two amyloid beta
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
 RT site.";
 RL J. Struct. Biol. 130:142-152(2000).
 RN [23]
 RP STRUCTURE BY NMR OF 681-706.
 RX MEDLINE=20400065; PubMed=10940221;
 RA Zhang S., Iwata K., Lachemann M.J., Peng J.W., Li S., Stimson E.R.,
 RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;
 RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in
 RT water.";
 RL J. Struct. Biol. 130:130-141(2000).
 RN [24]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.

DB 667 SEVKMDAEF 675

RESULT 10

AA_RAT STANDARD: PRT; 770 AA.

ID A4_RAT

AC P08592.

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog precursor

DE (Amyloidogenic glycoprotein) (AG).

GN APP.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.

RC TISSUE=Brain

RX MEDLINE=88312583; PubMed=2900758;

RA Shivers B.D., Hildich C., Muthaup G., Salbaum J.M., Beyreuther K., Seeburg P.H.;

RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.";

RT EMBO J. 7:1365-1370(1988).

RN [2]

RP SEQUENCE OF 289-364 FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=89183625; PubMed=2648331;

RA Kang J., Mueller-Hill B.;

RT "The sequence of the two extra exons in rat preA4.";

RT Nucleic Acids Res. 17:2130-2130(1989).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695), APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -1- SIMILARITY: CONTAINS 1 BPT1/KUNTZ INHIBITOR DOMAIN.

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CC EMBL; X07648; CAA30488.1; -

CC EMBL; X14066; CAA32229.1; -

CC PIR: S00550; S00550.

CC PIR: S03607; S03607.

CC HSP; P05067; 1AAP.

CC InterPro: IPR001868; A4_APP.

CC InterPro: IPR002223; Kuntz_BPT1.

CC Pfam: PF02177; A4_EXTRA; 1.

CC Pfam: PF00014; Kuntz_BPT1; 1.

CC PRINTS: PR00203; AMYLOIDA4.

CC PRINTS: PR00759; BASICTPASE.

CC SMART: SM00006; A4_EXTRA; 1.

CC SMART: SM00131; KU; 1.

CC PROSITE: PS00319; A4_EXTRA; 1.

CC PROSITE: PS00320; A4_INTRA; 1.

CC PROSITE: PS00280; BPT1_KUNTZ; 1.

CC PROSITE: PS50279; BPT1_KUNTZ; 2; 1.

CC Glycoprotein: Amyloid; Neurone; Transmembrane; Signal;

CC Alternative splicing; Serine protease inhibitor.

FT SIGNAL 1 17 BY SIMILARITY.

FT CHAIN 18 770 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN

FT DOMAIN 18 699 HOMOLOG.

FT TRANSMEM 700 723 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 724 770 POTENTIAL.

FT DOMAIN 673 715 CYTOSOLIC (POTENTIAL).

FT DOMAIN 673 715 EQUITALENT OF BETA-AMYLOID PROTEIN.

FT SITE 759 762 BPT1/KUNTZ INHIBITOR.

FT DISULFID 291 341 CLATHRIN-BINDING (BY SIMILARITY).

FT DISULFID 300 324 BY SIMILARITY.

FT DISULFID 316 337 BY SIMILARITY.

FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPPLIC 289 289 E -> V (IN ISOFORM APP(695)).

FT VARSPPLIC 290 364 MISSING (IN ISOFORM APP(695)).

SQ SEQUENCE 770 AA: 86704 MW: C26C9D6BB2D929A7 CRC64;

Query Match

Best Local Similarity 89.8%; Score 44; DB 1; Length 770;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEF 9

DB 667 SEVKMDAEF 675

QY 1 SEVKMDAEF 9

DB 667 SEVKMDAEF 675

RESULT 11

T2S1_STRFI

ID T2S1_STRFI STANDARD: PRT; 269 AA.

AC 052512;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Type II restriction enzyme SfiI (EC 3.1.21.4) (Endonuclease SfiI)

DE (K.SfiI).

DE SFIIR.

OS Streptomyces fimbriatus.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=68197;

RN [1]

RP SEQUENCE FROM N.A.

RA van Cott E.M., Moran L.S., Slatko B.E., Wilson G.G.;

RT "Characterization of the SfiI restriction and modification genes.";

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE GGCCNNNNNGCC AND CLEAVES BEFORE N-9.

CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give specific double-stranded fragments with terminal 5'-phosphates.

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CC EMBL; AF039750; AAB95365.1; -

CC DR RBASB; 1655; SfiI.

CC DR Hydrolase; Endonuclease; Nuclease; Restriction system.

CC KW SEQUENCE 269 AA: 31044 MW: 3C48499BAA5205EA CRC64;

Query Match

Best Local Similarity 75.5%; Score 37; DB 1; Length 269;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVKMDAEF 10

DB 115 SQPMDAEF 124

QY 1 SEVKMDAEF 10

DB 115 SQPMDAEF 124

RESULT 12

AC P04114; 000502; Q13787;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Apolipoprotein B-100 precursor (Apo B-100) [contains: Apolipoprotein
 B-48 (Apo B-48)].
 GN APOB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87016385; PubMed=3763409;
 RA Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
 RA Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
 RT "Complete cDNA and derived protein sequence of human apolipoprotein
 B-100.";
 RL Nucleic Acids Res. 14:7501-7503(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86803974; PubMed=3652907;
 RA Ludwig E.H., Blackhart B.D., Plerotti V.R., Caiati L., Fortier C.,
 RA Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
 RT "DNA sequence of the human apolipoprotein B gene.";
 RL DNA 6:363-372(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87008488; PubMed=3759943;
 RA Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
 RA Gotto A.M. Jr., Chan L.;
 RT "The complete cDNA and amino acid sequence of human apolipoprotein
 B-100.";
 RL J. Biol. Chem. 261:12918-12921(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87041416; PubMed=3464946;
 RA Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Jackner K.J.,
 RA Lee N., Brewer H.B. Jr.;
 RT "Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
 RT derived amino acid sequence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87161758; PubMed=3030729;
 RA Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.,
 RA Zannis V.I.;
 RT "The complete sequence and structural analysis of human
 RT apolipoprotein B-100: relationship between apob-100 and apob-48
 RT forms.";
 RL EMBO J. 5:3495-3507(1986).
 RN [6]
 RP SEQUENCE OF 709-906 FROM N.A.
 RX MEDLINE=85270450; PubMed=3660836;
 RA Deeb S.S., Motulsky A.G., Alpers J.J.;
 RT "A partial cDNA clone for human apolipoprotein B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985).
 RN [7]
 RP SEQUENCE OF 3056-3159 FROM N.A.
 RX MEDLINE=86041888; PubMed=3903660;
 RA Menhaden M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
 RA Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.;
 RT "Human apolipoprotein B: identification of cDNA clones and
 RT characterization of mRNA.";
 RL Nucleic Acids Res. 13:6937-6953(1985).
 RN [8]
 RP SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A.
 RX MEDLINE=86093680; PubMed=3841204;
 RA Carlsson P., Olofsson S.O., Bonders G., Darnfors C., Wiklund O.,
 RA Bjursell G.;
 RT "Molecular cloning of human apolipoprotein B cDNA.";
 RL Nucleic Acids Res. 13:8813-8826(1985).
 RN [9]

RP SEQUENCE OF 3109-4563 FROM N.A.
 RX MEDLINE=85300528; PubMed=2994225;
 RA Knott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.F.,
 RA Ureba M.S., Levy-Wilson B., Powell L.M., Pease R.J., Eddy R.,
 RA Nakai H., Byers M., Priestley L.W., Robertson E., Rall L.B.,
 RA Betsholtz C., Shows T.B., Mahley R.W., Scott J.;
 RT "Human apolipoprotein B: structure of carboxyl-terminal domains,
 RT sites of gene expression, and chromosomal localization.";
 RL Science 230:37-43(1985).
 RN [10]
 RP SEQUENCE OF 1-291 FROM N.A.
 RX MEDLINE=86149325; PubMed=3513177;
 RA Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
 RA Chen G.C., Kirsher S.W., McIntire G., Kane J.P.;
 RT "Isolation of a cDNA clone encoding the amino-terminal region of
 RT human apolipoprotein B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986).
 RN [11]
 RP SEQUENCE OF 1-1670 FROM N.A.
 RX MEDLINE=86287319; PubMed=3461454;
 RA Protter A.A., Hardman D.A., Sato K.Y., Schilling J.W.,
 RA Yamanaka M., Hori Y.J., Hjertild K.A., Chen G.C., Kane J.P.;
 RT "Analysis of cDNA clones encoding the entire B-26 region of human
 RT apolipoprotein B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986).
 RN [12]
 RP PARTIAL SEQUENCE, AND IDENTIFICATION (APO-B48).
 RX MEDLINE=88018019; PubMed=3659919;
 RA Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,
 RA Silberman S.R., Cai S.-J., Deslypere J.P., Rosseneu M.,
 RA Gotto A.M. Jr., Li W.-H., Chan L.;
 RT "Apolipoprotein B-48 is the product of a messenger RNA with an organ-
 RT specific in-frame stop codon.";
 RL Science 238:363-366(1987).
 RN [13]
 RP DOMAINS.
 RX MEDLINE=87039351; PubMed=3773997;
 RA Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,
 RA Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
 RA Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,
 RA Levy-Wilson B., Scott J.;
 RT "Complete protein sequence and identification of structural domains
 RT of human apolipoprotein B.";
 RL Nature 323:734-738(1986).
 RN [14]
 RP DOMAINS.
 RA Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T.,
 RA Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M.,
 RA Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L.;
 RT "Sequence, structure, receptor-binding domains and internal repeats
 RT of human apolipoprotein B-100.";
 RL Nature 323:738-742(1986).
 RN [15]
 RP CALCIUM-BINDING DATA.
 RX MEDLINE=86242245; PubMed=3087360;
 RA Dashti N., Lee D.M., Mok T.;
 RT "Apolipoprotein B is a calcium binding protein.";
 RL Biochem. Biophys. Res. Commun. 137:493-499(1986).
 RN [16]
 RP VARIANT SER-4338.
 RX MEDLINE=91071750; PubMed=1979313;
 RA Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P.,
 RA Cuny G., Cambien F., Rolzes G.;
 RT "Detection by denaturing gradient gel electrophoresis of a new
 RT polymorphism in the apolipoprotein B gene.";
 RL Hum. Genet. 86:91-93(1990).
 RN [17]
 RP VARIANT FDB GLN-3527.
 RX MEDLINE=89098975; PubMed=2563166;
 RA Sorla L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
 RA McCarthy B.J.;
 RT "Association between a specific apolipoprotein B mutation and
 RT familial defective apolipoprotein B-100.";

Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
 [18]
 RP VARIANT LEU-2739. PubMed=2216805;
 RX MEDLINE=91016974; PubMed=2216805;
 RA Huang L.-S., Gavish D., Breslow J.L.;
 RT "Sequence polymorphism in the human apob gene at position 8344.";
 RL Nucleic Acids Res. 18:5922-5923(1990).
 RN [19]
 RP VARIANT FDB CYS-3558.
 RX MEDLINE=95190020; PubMed=7883971;
 RA Pullinger C.R., Hennessey L.K., Chatterton J.E., Liu W., Love J.A.,
 RA Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.;
 RT "Familial ligand-defective apolipoprotein B. Identification of a new
 mutation that decreases LDL receptor binding affinity.";
 RL J. Clin. Invest. 95:1225-1234(1995).
 RN [20]
 RP VARIANTS L-1437; S-1914; K-2566; T-3121; A-3945; M-4128 AND T-4481.
 RX MEDLINE=97044521; PubMed=8889592;
 RA Polier O., Ricard S., Behague I., Souriau C., Evans A.E.,
 RA Arveiler D., Marques-Vidal P., Luc G., Roizes G., Camdien F.;
 RT "Detection of new variants in the apolipoprotein B (Apo B) gene by
 PCR-SSCP.";
 RL Hum. Mutat. 8:282-285(1996).
 RN [21]
 RP VARIANTS FDB GLN-3527 AND CYS-3558.
 RX MEDLINE=97403938; PubMed=9259199;
 RA Rades J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G.,
 RA Krempf M., Giraudet P., Junien C., Boileau C.;
 RT "Familial ligand-defective apolipoprotein B-100: simultaneous
 detection of the ARG3500->GLN and ARG3531->CYS mutations in a
 French population.";
 RL Hum. Mutat. 10:160-163(1997).
 RN [22]
 RP VARIANTS S-1914; R-1923; L-2739; D-3319; T-3427; Q-3432 AND I-3921.
 RX MEDLINE=98141125; PubMed=9490296;
 RA Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;
 RT "Screening for mutations of the apolipoprotein B gene causing
 hypocholesterolemia.";
 RL Hum. Genet. 102:44-49(1998).
 CC -1- FUNCTION: APOLOPROTEIN B IS A MAJOR PROTEIN CONSTITUENT OF
 CHYLOMICRONS, VLDL AND LDL. IT FUNCTIONS AS A RECOGNITION SIGNAL
 FOR THE CELLULAR BINDING AND INTERNALIZATION OF LDL PARTICLES BY
 THE APOB/E RECEPTOR.
 CC -1- DISEASE: DEFECTS IN APOB ARE A CAUSE OF FAMILIAL LIGAND-DEFECTIVE
 APOLOPROTEIN B-100 (FDB). IT IS A DOMINANTLY INHERITED DISORDER
 OF LIPOPROTEIN METABOLISM LEADING TO HYPERCHOLESTEROLEMIA AND
 INCREASED PRONENESS TO CORONARY ARTERY DISEASE (CAD).
 CC THE PLASMA CHOLESTEROL LEVELS ARE DRAMATICALLY ELEVATED DUE TO
 IMPAIRED CLEARANCE OF LDL PARTICLES BY DEFECTIVE APOB/E RECEPTORS.
 CC -1- DISEASE: DEFECTS IN APOB ASSOCIATED WITH OTHER GENE DEFECTS
 (POLYGENIC) CAN BE THE CAUSE OF HYPOCHOLESTEROLEMIA.
 CC -1- MISCELLANEOUS: APO B-48 WHICH IS SYNTHESIZED ONLY BY THE
 INTESTINE, AND FOUND IN CHYLOMICRONS, IS A SHORTENED FORM OF APO
 B.
 Query Match 69.4%; Score 34; DB 1; Length 4563;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 EVKMDAER 10
 DB 1483 EVKIDGQR 1491
 RESULT 14
 CC15_SCHPO STANDARD; PRT; 927 AA.
 AC 009822; 014365;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cell division control protein 15.
 GN CDC15 OR SPAC2068.05C.
 OS Schizosaccharomyces pombe (fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=95360987; PubMed=7634333;
 RA Fankhauser C., Raymond A., Cerutti L., Utzig S., Hofmann K.;
 RA Fankhauser C., Raymond A., Cerutti L., Utzig S., Hofmann K.;
 RT "The S. pombe cdc15 gene is a key element in the reorganization of F-
 actin at mitosis.";
 RL Cell 82:435-444(1995).
 RN [2]
 RP REVISIONS TO N-TERMINUS.
 RA Fankhauser C., Raymond A., Cerutti L., Utzig S., Hofmann K.;
 RA Fankhauser C., Raymond A., Cerutti L., Utzig S., Hofmann K.;
 RT Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Badcock K., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases
 CC -1- FUNCTION: AFTER THE ONSET OF MITOSIS, FORMS A RING-LIKE STRUCTURE
 WHICH CO-LOCALIZES WITH THE MEDIAL ACTIN RING. APPEARS TO MEDIAL
 CYTOSKELETAL REARRANGEMENTS REQUIRED FOR CYTOKINESIS. ESSENTIAL
 FOR VIABILITY.
 CC -1- DEVELOPMENTAL STAGE: PEAKS IN EARLY MITOSIS BEFORE SEPTATION.
 CC -1- DOMAIN: THE N-TERMINAL REGION IS IN A COILED COIL STRUCTURE.
 CC -1- PTM: PHOSPHORYLATED.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -1- SIMILARITY: SOME, TO S.POMBE SPB11C11.02 AND SPAC7D4.02C.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X86179; CA60115.1; -;
 DR EMBL; Z95334; CAB08599.2; -;
 DR HSSP; P07751; ITUD.
 DR InterPro; IPR001060; FCH.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00611; FCH; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR SMART; SM00055; FCH; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR KWSite; Cytoskeleton; SH3 domain; Phosphorylation; Coiled coil.
 FT DOMAIN 24 110 FCH.
 FT DOMAIN 108 207 COILED COIL (POTENTIAL).
 FT DOMAIN 866 927 SH3.
 FT SEQUENCE 927 AA; 102119 MW; FDCET7E0AAA3D247D CR664;
 Query Match 67.3%; Score 33; DB 1; Length 927;
 Best Local Similarity 85.7%; Pred. No. 48;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 KMDAER 10
 DB 195 KMDAER 201
 RESULT 15
 Y683_HALN1 STANDARD; PRT; 263 AA.
 ID Y683_HALN1
 AC 09HR12;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

```

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative aldolase Yng0683c (EC 4.2.1.-).
GN YNG0683C.
OS Halobacterium sp. (strain NRC-1).
OC Archaea: Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahatas G.G., Bergquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Bailga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weil D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leitnauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isebnarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Epphardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RA "genome sequence of Halobacterium species NRC-1."
RA Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
RL
CC -1- SIMILARITY: BELONGS TO THE DEOC/FRAB FAMILY OF ALDOLASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: AE005014; AA619176.1;
CC KW Hypothetical protein; Lyase; Schiff base; Complete proteome.
CC FT BINDING 177 177 SCHIFF-BASE (BY SIMILARITY).
CC SO SEQUENCE 263 AA; 28083 MW; 25FF044B6A77494F CRC64;
CC -----
QY 1 SEVKMDAEFR 10
   111:1 111
Db 119 SEVEMAEFR 128

```

Search completed: October 29, 2002, 10:27:28
 Job time : 6 secs

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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:11 ; Search time 18 Seconds
(without alignments)
96.108 Million cell updates/sec

Title: US-09-580-018-4
Perfect score: 49
Sequence: 1 SEVKMDAEFR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.19:**
1: sp.archaea:**
2: sp.bacteria:**
3: sp.fungi:**
4: sp.human:**
5: sp.invertebrate:**
6: sp.mammal:**
7: sp.mmc:**
8: sp.organelle:**
9: sp.phage:**
10: sp.plant:**
11: sp.protozoan:**
12: sp.virus:**
13: sp.invertebrate:**
14: sp.unclassified:**
15: sp.virus:**
16: sp.bacteriophage:**
17: sp.archaea:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	49	100.0	82	4	P78438	P78438 homo sapien
2	49	100.0	82	4	016014	016014 homo sapien
3	49	100.0	82	4	016019	016019 homo sapien
4	49	100.0	82	4	016020	016020 homo sapien
5	49	100.0	534	13	093296	093296 gallus gall
6	49	100.0	569	13	093296	093296 gallus gall
7	49	100.0	695	6	093296	093296 gallus gall
8	49	100.0	695	6	093296	093296 gallus gall
9	49	100.0	695	11	060496	060496 cavia sp. P
10	49	100.0	695	13	093296	093296 gallus gall
11	49	100.0	770	6	093296	093296 gallus gall
12	44	89.8	79	11	035463	035463 sus scrofa
13	44	89.8	607	11	099K32	099K32 mus musculus
14	44	89.8	695	11	P97487	P97487 mus musculus
15	43	87.8	693	13	098SG0	098SG0 xenopus lae
16	43	87.8	695	13	098SF9	098SF9 xenopus lae

17	43	87.8	747	13	091963	091963 xenopus. ap
18	42	85.7	423	2	052379	052379 raietonia s
19	42	85.7	423	2	045693	045693 burkholderi
20	39	79.6	142	5	016896	016896 caenorhabdi
21	36	73.5	630	2	0931K4	0931K4 vibrio sp.
22	35	71.4	317	17	0962T2	0962T2 sulfolobus
23	35	71.4	774	16	092CV7	092CV7 listeria in
24	34	69.4	239	10	09FMC2	09FMC2 streptomyces
25	34	69.4	605	2	09LIF6	09LIF6 arabidopsis
26	34	69.4	1192	10	094BS1	094BS1 arabidopsis
27	34	69.4	1261	10	094L30	094L30 arabidopsis
28	34	69.4	3262	4	013788	013788 homo sapien
29	33	67.3	302	9	037840	037840 bacterioph
30	33	67.3	438	2	09A1K4	09A1K4 biophila w
31	33	67.3	621	4	09H9T1	09H9T1 homo sapien
32	33	67.3	1027	4	09BMX2	09BMX2 homo sapien
33	33	67.3	1245	10	09C7F8	09C7F8 arabidopsis
34	32	65.3	143	4	09H935	09H935 homo sapien
35	32	65.3	161	16	098FE22	098FE22 rhizobium l
36	32	65.3	338	2	09A167	09A167 chlorobium
37	32	65.3	340	5	09U0X8	09U0X8 leishmania
38	32	65.3	350	2	09AL73	09AL73 chlorobium
39	32	65.3	350	2	09AL69	09AL69 chlorobium
40	32	65.3	350	2	09AL72	09AL72 chlorobium
41	32	65.3	376	12	09DVZ3	09DVZ3 plutella xy
42	32	65.3	405	4	09BU21	09BU21 homo sapien
43	32	65.3	426	17	09V2P8	09V2P8 pyrococcus
44	32	65.3	539	4	09NWD6	09NWD6 homo sapien
45	32	65.3	539	4	09NM45	09NM45 homo sapien

ALIGNMENTS

RESULT 1
P78438 PRELIMINARY; PRT; 82 AA.
ID P78438
AC P78438;
DT 01-MAY-1997 (TREMREL. 03, Created)
DT 01-MAY-1997 (TREMREL. 03, Last sequence update)
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8932030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor."
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [2]
RP SEQUENCE OF 19-48 FROM N.A.
RX MEDLINE=87120329; PubMed=2949367;
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;
RT "Amyloid beta protein gene: CDNA, mRNA distribution, and genetic
RT linkage near the Alzheimer locus."
RL Science 235:880-884(1987).
RN [3]
RP SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE=9305397; PubMed=1415269;
RA Kamito K., Orr H.T., Payami H., Wajsmann E.M., Alonso M.E., Pulst S.M.,
RA Anderson L., O'dahl S., Nemens E., White J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease
RT kindreds for the APP gene region."
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL: M29270; AAA51768.1; JOINED.
EMBL: M29269; AAA51768.1; JOINED.

DR EMBL; M15532; AAA51564.1; -.
 DR EMBL; S45136; AAB23646.1; -.
 DR HSSP; P05067; 1BA4. 1
 FT NON_TER 1
 SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match 100.0%; Score 49; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 0.009;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10
 |||||
 Db 12 SEVKMDAEFR 21

RESULT 2

ID Q16014 PRELIMINARY; PRT; 82 AA.
 AC Q16014;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE BETA-AMYL0ID PEPTIDE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93236601; PubMed-8476439;
 RA Denman R.B., Rosenzweig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).

DR EMBL; S60721; AAB26265.2; -.
 DR HSSP; P05067; 1BA4. 1
 FT NON_TER 1
 SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 49; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 0.009;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10
 |||||
 Db 13 SEVKMDAEFR 22

RESULT 3

ID Q16019 PRELIMINARY; PRT; 82 AA.
 AC Q16019;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE BETA-AMYL0ID PEPTIDE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93236601; PubMed-8476439;
 RA Denman R.B., Rosenzweig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).

DR EMBL; S61380; AAB26264.2; -.
 DR HSSP; P05067; 1BA4. 1
 FT NON_TER 1
 SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 100.0%; Score 49; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 0.009;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10
 |||||
 Db 13 SEVKMDAEFR 22

RESULT 4

ID Q16020 PRELIMINARY; PRT; 82 AA.
 AC Q16020;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE BETA-AMYL0ID PEPTIDE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93236601; PubMed-8476439;
 RA Denman R.B., Rosenzweig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).

DR EMBL; S61383; AAB26265.2; -.
 DR HSSP; P05067; 1BA4. 1
 FT NON_TER 1
 SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 100.0%; Score 49; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 0.009;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10
 |||||
 Db 13 SEVKMDAEFR 22

RESULT 5

ID O93296 PRELIMINARY; PRT; 534 AA.
 AC O93296;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE AMYL0ID PROTEIN (FRAGMENT).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98337885; PubMed-9671674;
 RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
 RA Milligan C.E.;
 RT "Increased production of amyloid precursor protein provides a
 substrate for caspase-3 in dying motoneurons.";
 RL J. Neurosci. 18:5869-5880(1998).

DR EMBL; AF042098; AAC25052.1; -.
 DR HSSP; P05067; 1BA4.
 DR Interpro: IPR001868; A4 APP.
 DR PRINTS: PR00203; AMYL0ID4.
 DR PROSITE: PS00319; A4-EXTRA; 1.
 DR PROSITE: PS00320; A4-INTRA; 1.

FT	NON_TER	1	1	
SO	SEQUENCE	534 AA;	60597 MW;	FB53EC2E66D4C92 CRC64;
Query Match				
	Best Local Similarity	100.0%;	Score 49;	DB 13; Length 534;
	Matches 10;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1 SEVKMDAEFR 10			
DB	431 SEVKMDAEFR 440			
RESULT 6				
ID	09PVL1	PRELIMINARY;	PRT:	569 AA.
AC	09PVL1			
DT	01-MAY-2000 (TREMBLrel. 13,	Created)		
DT	01-MAY-2000 (TREMBLrel. 13,	Last sequence update)		
DE	01-DEC-2001 (TREMBLrel. 19,	Last annotation update)		
DE	AMYL0ID PROTEIN (FRAGMENT).			
GN	App.			
OS	Gallus gallus (Chicken).			
OC	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BRAIN;			
RA	Coulson E.J., Paliaga K., Beyreuther K., Masters C.L.;			
RT	"What the evolution of the amyloid protein precursor supergene family			
RT	tells us about its function."			
RL	Neurochem. Int. 0:0-(2000).			
DR	EMBL; AF030341; AAF12698.1; -			
DR	HSSP; P05067; 1BA4.			
DR	InterPro; IPR001868; A4_APP.			
DR	Pfam; PF02177; A4_EXTRA; 1.			
DR	PRINTS; PRO0203; AMYLOIDA4.			
DR	SMART; SM00006; A4_EXTRA; 1.			
DR	PROSITE; PS00319; A4_EXTRA; 1.			
DR	PROSITE; PS00320; A4_INTRA; 1.			
FT	NON_TER	1		
SO	SEQUENCE	569 AA;	64753 MW;	0AB8BB851863A19D CRC64;
Query Match				
	Best Local Similarity	100.0%;	Score 49;	DB 13; Length 569;
	Matches 10;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1 SEVKMDAEFR 10			
DB	467 SEVKMDAEFR 476			
RESULT 7				
ID	095KN7	PRELIMINARY;	PRT:	695 AA.
AC	095KN7			
DT	01-DEC-2001 (TREMBLrel. 19,	Created)		
DT	01-DEC-2001 (TREMBLrel. 19,	Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19,	Last annotation update)		
DE	AMYL0ID B-PROTEIN PRECURSOR.			
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;			
OC	Cercopithecinae; Macaca.			
OX	NCBI_TaxID=9541;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=CEREBELLUM;			
RC	MEDLINE=91273117; PubMed=1905108;			
RA	Podlinsky M.B., Tolan D.R., Selkoe D.J.;			
RT	"Homology of the amyloid beta protein precursor in monkey and human			
RT	supports a primate model for beta amyloidosis in Alzheimer's			

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RT disease." ;
RT Am. J. Pathol. 138:1423-1425(1991) .
DR EMBL: M58727; AAA36829.1; -.
FT SIGNAL 17 POTENTIAL.
FT CHAIN 597 636 POTENTIAL.
SQ SEQUENCE 695 AA; 78663 MW; 4F5EA019F969D56 CRC64;

Query Match
Best Local Similarity 100.0%; Score 49; DB 6; Length 695;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEFR 10
Db 592 SEVKMDAEFR 601
|||||||

RESULT 8
Q60496 PRELIMINARY; PRT; 695 AA.
AC Q60496;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE AMYLOID PRECURSOR PROTEIN.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing.";
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL: X97631; CA66230.1; -.
DR HSSP; P05067; 1BA4
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PRO0203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F15AB CRC64;

Query Match
Best Local Similarity 100.0%; Score 49; DB 11; Length 695;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEFR 10
Db 592 SEVKMDAEFR 601
|||||||

RESULT 9
Q9DGJ8 PRELIMINARY; PRT; 695 AA.
AC Q9DGJ8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archaeoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Satasa M., Rodolosse A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms." ;

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RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289218; AAG0593.1; -.
DR HSSP: P03067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match
Best Local Similarity 100.0%; Score 49; DB 13; Length 695;
Pred. No. 0.079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAER 10
DB 592 SEVKMDAER 601

RESULT 10
Q9DGJ7 PRELIMINARY; PRT; 751 AA.
AC Q9DGJ7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolose A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289219; AAG0594.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match
Best Local Similarity 100.0%; Score 49; DB 13; Length 751;
Pred. No. 0.085;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAER 10
DB 648 SEVKMDAER 657

RESULT 11
Q9TUI0 PRELIMINARY; PRT; 770 AA.
AC Q9TUI0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

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OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid Precursor Protein 770."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB032550; BAA84580.1; -.
DR HSSP: P05067; 1AAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DC82BCC583E CRC64;

Query Match
Best Local Similarity 100.0%; Score 49; DB 6; Length 770;
Pred. No. 0.088;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAER 10
DB 667 SEVKMDAER 676

RESULT 12
O35463 PRELIMINARY; PRT; 79 AA.
ID O35463;
AC O35463;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).
GN BETA APP.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Sambamurti K., Pinnix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF030413; AAB86608.1; -.
DR HSSP: P05067; 1BA4.
FT NON_TER 1
FT NON_TER 79
FT NON_TER 79
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match
Best Local Similarity 100.0%; Score 44; DB 11; Length 79;
Pred. No. 0.097;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAER 9
DB 16 SEVKMDAER 24

RESULT 13
Q99K32 PRELIMINARY; PRT; 607 AA.
ID Q99K32;
AC Q99K32;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL 68.4 KDA PROTEIN (FRAGMENT).

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR. MAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RC TISSUE.
RA Strausberg R.;
RU Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005490; AAH05490.1; -.
DR HSSP; P05067; 1AAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00280; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KM Hypothetical protein; Serine protease inhibitor.
FT NON_TER
SQ SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;

Query Match 89.8%; Score 44; DB 11; Length 607;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEF 9
Db 504 SEVKMDAEF 512

RESULT 14
P97487 PRELIMINARY; PRT; 695 AA.
AC P97487; P97942;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HIPPOCAMPAL AMYLOID PROTEIN.
CN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SAMP8; TISSUE=HIPPOCAMPUS;
RA Flood J.F., Kumar V.B., Sasser T., Word I., Morley J.F.;
RU Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 581-662 FROM N.A.
RC STRAIN=129SV;
RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecci M.,
RA Loring J.F., Goate A.M.;
RU Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U84012; AAB41502.1; -.
DR EMBL; U82624; AAB40919.1; -.
DR HSSP; P05067; 1MMP.
DR MGD; MGI:86059; APP.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78414 MW; 9A5FB2ED261236E CRC64;

Query Match 89.8%; Score 44; DB 11; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.88;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEF 9
Db 592 SEVKMDAEF 600

RESULT 15
O98SGO PRELIMINARY; PRT; 693 AA.
ID O98SGO
AC O98SGO;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN A.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OX Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RU Thesis (2001), Department of Biological Sciences,
RU University of Nijmegen, Nijmegen, Netherlands.
DR EMBL; AJ296150; CAC37193.1; -.
DR HSSP; P05067; 1H23.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KM Signal.
FT SIGNAL
SQ SEQUENCE 693 AA; 78568 MW; CAF1DF555C1AB653 CRC64;

Query Match 87.8%; Score 43; DB 13; Length 693;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEF 10
Db 590 SEVKMDSEFR 599

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Search completed: October 29, 2002, 10:29:41
 Job time : 19.1429 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:56 ; Search time 9 Seconds
(without alignments)
27.140 Million cell updates/sec

Title: US-09-580-018-4
Perfect score: 49
Sequence: 1 SEVMDAEFR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA: *
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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCrUS.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/Backfill1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	49	100.0	12	5	PCT-US94-07043A-2
3	49	100.0	16	5	PCT-US94-07043A-1
4	49	100.0	27	1	US-08-141-324-11
5	49	100.0	27	1	US-08-541-902-11
6	49	100.0	45	1	US-08-462-859A-5
7	49	100.0	45	1	US-08-123-659A-5
8	49	100.0	45	1	US-08-464-247A-5
9	49	100.0	45	1	US-08-464-248A-5
10	49	100.0	58	1	US-08-371-930-25
11	49	100.0	58	5	PCT-US94-01712-25
12	49	100.0	63	1	US-08-462-859A-3
13	49	100.0	63	1	US-08-462-859A-4
14	49	100.0	63	1	US-08-123-659A-3
15	49	100.0	63	1	US-08-123-659A-4
16	49	100.0	63	1	US-08-464-247A-3
17	49	100.0	63	1	US-08-464-247A-4
18	49	100.0	63	1	US-08-464-248A-3
19	49	100.0	63	1	US-08-464-248A-4
20	49	100.0	105	2	US-08-729-345-1
21	49	100.0	117	2	US-08-729-345-3
22	49	100.0	152	6	5187153-4
23	49	100.0	162	6	5220013-4
24	49	100.0	162	6	5223482-4
25	49	100.0	264	1	US-07-990-893-5
26	49	100.0	487	1	US-08-462-859A-9
27	49	100.0	487	1	US-08-123-659A-9

28	49	100.0	487	1	US-08-464-247A-9	Sequence 9, Appli
29	49	100.0	487	1	US-08-464-248A-9	Sequence 9, Appli
30	49	100.0	492	1	US-08-462-859A-7	Sequence 7, Appli
31	49	100.0	492	1	US-08-123-659A-7	Sequence 7, Appli
32	49	100.0	492	1	US-08-464-247A-7	Sequence 7, Appli
33	49	100.0	492	1	US-08-464-248A-7	Sequence 7, Appli
34	49	100.0	537	1	US-08-453-552-4	Sequence 4, Appli
35	49	100.0	537	2	US-08-710-637-4	Sequence 4, Appli
36	49	100.0	537	5	PCT-US93-00907-4	Sequence 4, Appli
37	49	100.0	656	1	US-08-371-930-23	Sequence 23, Appli
38	49	100.0	656	5	PCT-US94-01712-23	Sequence 23, Appli
39	49	100.0	676	1	US-08-371-930-24	Sequence 24, Appli
40	49	100.0	676	5	PCT-US94-01712-24	Sequence 24, Appli
41	49	100.0	694	1	US-08-339-152A-18	Sequence 18, Appli
42	49	100.0	694	2	US-08-007-999B-5	Sequence 5, Appli
43	49	100.0	694	2	US-08-689-276A-5	Sequence 5, Appli
44	49	100.0	695	1	US-08-371-930-27	Sequence 27, Appli
45	49	100.0	695	1	US-08-123-702-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
PCT-US94-07043A-7
Sequence 7, Application PC/TUS9407043A
GENERAL INFORMATION:
APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,
APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard
TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC
TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miles Inc.
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
COMPUTER: Sharp PC 4600
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07043A
FILING DATE: June 21, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10889
FILING DATE: November 12, 1993
PRIOR APPLICATION DATA: 07/995,660
APPLICATION NUMBER: December 16, 1992
FILING DATE: May 11, 1992
APPLICATION NUMBER: 07/880,914
ATTORNEY/AGENT INFORMATION:
NAME: Pamela A. Simonton
REGISTRATION NUMBER: 31,060
REFERENCE/DOCKET NUMBER: MTI 224.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 937-2340
TELEFAX: (203) 937-2795
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-07043A-7
Query Match 100.0%; Score 49; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00045;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10
 |||||||||

Db 2 SEVKMDAEFR 11

RESULT 2
 PCT-US94-07043A-2
 ; Sequence 2, Application PC/TUS9407043A
 ; GENERAL INFORMATION:
 ; APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,
 ; APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard
 ; TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC
 ; TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Miles Inc.
 ; STREET: 400 Morgan Lane
 ; CITY: West Haven
 ; STATE: Connecticut
 ; COUNTRY: USA
 ; ZIP: 06516
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
 ; COMPUTER: Sharp PC 4600
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: Wordperfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/07043A
 ; FILING DATE: June 21, 1994
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/10889
 ; FILING DATE: November 12, 1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/995,660
 ; FILING DATE: December 16, 1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/880,914
 ; FILING DATE: May 11, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pamela A. Simonton
 ; REGISTRATION NUMBER: 31,060
 ; REFERENCE/DOCKET NUMBER: MTI 224.3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (203) 937-2340
 ; TELEFAX: (203) 937-2795
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 12 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; PCT-US94-07043A-2

Query Match 100.0%; Score 49; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0005;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10
 |||||||||

Db 2 SEVKMDAEFR 11

RESULT 3
 PCT-US94-07043A-1
 ; Sequence 1, Application PC/TUS9407043A
 ; GENERAL INFORMATION:
 ; APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,
 ; APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard
 ; TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC
 ; TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE
 ; NUMBER OF SEQUENCES: 11

;; CORRESPONDENCE ADDRESS:
 ;; ADDRESSEE: Miles Inc.
 ;; STREET: 400 Morgan Lane
 ;; CITY: West Haven
 ;; STATE: Connecticut
 ;; COUNTRY: USA
 ;; ZIP: 06516
 ;; COMPUTER READABLE FORM:
 ;; MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
 ;; COMPUTER: Sharp PC 4600
 ;; OPERATING SYSTEM: MS-DOS
 ;; SOFTWARE: Wordperfect 5.1
 ;; CURRENT APPLICATION DATA:
 ;; APPLICATION NUMBER: PCT/US94/07043A
 ;; FILING DATE: June 21, 1994
 ;; CLASSIFICATION:
 ;; PRIOR APPLICATION DATA:
 ;; APPLICATION NUMBER: PCT/US93/10889
 ;; FILING DATE: November 12, 1993
 ;; PRIOR APPLICATION DATA:
 ;; APPLICATION NUMBER: 07/995,660
 ;; FILING DATE: December 16, 1992
 ;; PRIOR APPLICATION DATA:
 ;; APPLICATION NUMBER: 07/880,914
 ;; FILING DATE: May 11, 1992
 ;; ATTORNEY/AGENT INFORMATION:
 ;; NAME: Pamela A. Simonton
 ;; REGISTRATION NUMBER: 31,060
 ;; REFERENCE/DOCKET NUMBER: MTI 224.3
 ;; TELECOMMUNICATION INFORMATION:
 ;; TELEPHONE: (203) 937-2340
 ;; TELEFAX: (203) 937-2795
 ;; INFORMATION FOR SEQ ID NO: 1:
 ;; SEQUENCE CHARACTERISTICS:
 ;; LENGTH: 16 amino acids
 ;; TYPE: amino acid
 ;; TOPOLOGY: linear
 ;; PCT-US94-07043A-1

Query Match 100.0%; Score 49; DB 5; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.00067;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAEFR 10
 |||||||||

Db 2 SEVKMDAEFR 11

RESULT 4
 US-08-141-324-11
 ; Sequence 11, Application US/08141324
 ; Patent No. 5475097
 ; GENERAL INFORMATION:
 ; APPLICANT: Travis, James
 ; APPLICANT: Potempa, Jan S.
 ; APPLICANT: Barr, Philip J.
 ; APPLICANT: Pavloff, Nadine
 ; APPLICANT: Pike, Robert N.
 ; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
 ; TITLE OF INVENTION: Protease
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Greenlee and Winner, P. C.
 ; STREET: 5370 Manhattan Circle, Suite 201
 ; CITY: Boulder
 ; STATE: CO
 ; COUNTRY: US
 ; ZIP: 80303
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/141,324
;; FILING DATE: 21-OCT-1993
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ferber, Donna M.
;; REGISTRATION NUMBER: 33,878
;; REFERENCE/DOCKET NUMBER: 44-93
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 303-499-8080
;; TELEFAX: 303-499-8089
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 27 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHEICAL: NO
;; ANTI-SENSE: NO
US-08-141-324-11

Query Match 100.0%; Score 49; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
|||
Db 4 SEVKMDAEFR 13

RESULT 5
US-08-541-902-11
; Sequence 11, Application US/08541902
; Patent No. 5707620
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,902
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids

;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHEICAL: NO
;; ANTI-SENSE: NO
US-08-541-902-11

Query Match 100.0%; Score 49; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
|||
Db 4 SEVKMDAEFR 13

RESULT 6
US-08-462-859A-5
; Sequence 5, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3305
; TELEFAX: (201)831-3246
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-859A-5

Query Match 100.0%; Score 49; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAEFR 10
|||
Db 5 SEVKMDAEFR 14

RESULT 7
US-08-123-659A-5
; Sequence 5, Application US/08123659A
; Patent No. 5656477

GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-5

Query Match 100.0%; Score 49; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEPFR 10
|||||
DB 5 SEVKMDAEPFR 14

RESULT 8
US-08-464-247A-5
Sequence 5, Application US/08464247A
Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-5

Query Match 100.0%; Score 49; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVKMDAEPFR 10
|||||
DB 5 SEVKMDAEPFR 14

RESULT 9
US-08-464-248A-5
Sequence 5, Application US/08464248A
Patent No. 5703209
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne New Jersey
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-5

Query Match 100.0%; Score 49; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAER 10
DB 5 SEVKMDAER 14

RESULT 10

US-08-371-930-25
; Sequence 25, Application US/08371930
; Patent No. 5578451
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuro
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,930
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-371-930-25

Query Match

100.0%; Score 49; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAER 10
DB 42 SEVKMDAER 51

RESULT 11

PCT-US94-01712-25
; Sequence 25, Application PC/TUS9401712
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuro
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/019,208
FILING DATE: February 18, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/154001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 58
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US94-01712-25

Query Match 100.0%; Score 49; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVKMDAER 10
DB 42 SEVKMDAER 51

RESULT 12

US-08-462-859A-3
; Sequence 3, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; OF B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid

STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-462-859A-3

Query Match
 Best Local Similarity 100.0%; Score 49; DB 1; Length 63;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAER 10
 Db 5 SEVKMDAER 14

RESULT 13
 US-08-462-859A-4
 Sequence 4, Application US/08462859A

GENERAL INFORMATION:
 APPLICANT: Jacobsen, J. S.
 TITLE OF INVENTION: NO. 5652092el Amyloid Precursor and Method of
 TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
 TITLE OF INVENTION: of B-Amyloid Peptide
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: American Cyanamid Company
 STREET: One Cyanamid Plaza
 CITY: Wayne
 STATE: New Jersey
 COUNTRY: United States
 ZIP: 07470-8426

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/462,859A
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Barnhard, Elizabeth M.
 REGISTRATION NUMBER: 31,088
 REFERENCE/DOCKET NUMBER: 31,844-04
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201)831-3246
 TELEFAX: (201)831-3305
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 63 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-462-859A-4

Query Match
 Best Local Similarity 100.0%; Score 49; DB 1; Length 63;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAER 10
 Db 5 SEVKMDAER 14

RESULT 14
 US-08-123-659A-3
 Sequence 3, Application US/08123659A

GENERAL INFORMATION:
 APPLICANT: Jacobsen, J. S.
 ATTORNEY/AGENT INFORMATION:
 NAME: Vittek, M. P.

TITLE OF INVENTION: NO. 5656477el Amyloid Precursor and Method of
 TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
 TITLE OF INVENTION: of B-Amyloid Peptide
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Anne Rosenblum
 STREET: 163 Delaware Avenue, Suite 212
 CITY: Delmar
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 12054

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/123,659A
 FILING DATE: 20-SEP-1993
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Rosenblum, Anne M.
 REGISTRATION NUMBER: 30,419
 REFERENCE/DOCKET NUMBER: 31,844-01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (518)475-0611
 TELEFAX: (518)475-0619
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 63 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match
 Best Local Similarity 100.0%; Score 49; DB 1; Length 63;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVKMDAER 10
 Db 5 SEVKMDAER 14

RESULT 15
 US-08-123-659A-4
 Sequence 4, Application US/08123659A

GENERAL INFORMATION:
 APPLICANT: Jacobsen, J. S.
 TITLE OF INVENTION: NO. 5656477el Amyloid Precursor and Method of
 TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
 TITLE OF INVENTION: of B-Amyloid Peptide
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Anne Rosenblum
 STREET: 163 Delaware Avenue, Suite 212
 CITY: Delmar
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 12054

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/123,659A
 FILING DATE: 20-SEP-1993
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Rosenblum, Anne M.

REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-4

Query Match 100.0%; Score 49; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEYKMDAER 10
 |||||
Db 5 SEYKMDAER 14

Search completed: October 29, 2002, 10:32:07
Job time : 9 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:21 ; Search time 23.1429 Seconds
(without alignments)
47.995 Million cell updates/sec

Title: US-09-580-018-5
Perfect score: 53
Sequence: 1 EYKMDAEPFH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
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21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	53	100.0	10	22	AAAB6209	Human APP derived
2	53	100.0	13	19	AAW70869	Beta-amyloid pepti
3	53	100.0	16	21	AAAB06315	Human beta-amyloid
4	53	100.0	16	21	AAAB06317	Human beta-amyloid
5	53	100.0	18	22	AAE00608	Beta-amyloid precu
6	53	100.0	19	12	AAE14135	Brain-derived prot
7	53	100.0	20	21	AAE69713	Beta-APP alpha-sec
8	53	100.0	33	20	AAW98002	Amyloid precursor
9	53	100.0	39	21	AAE69717	Beta-APP alpha-sec
10	53	100.0	45	18	AAW26512	Amyloid precursor
11	53	100.0	45	18	AAW26392	Amyloid precursor

12	53	100.0	45	19	AAW44748	APP-REP 751 [BAP d
13	53	100.0	45	19	AAW42977	Deletion beta-amy1
14	53	100.0	53	15	AAE55695	Sequence of uniden
15	53	100.0	53	15	AAE55696	Sequence of uniden
16	53	100.0	53	15	AAE55697	Sequence of uniden
17	53	100.0	53	16	AAE64168	Variant beta amylo
18	53	100.0	54	21	AAE32126	Amyloid-beta precu
19	53	100.0	57	21	AAE10910	Human amyloid prec
20	53	100.0	58	15	AAE58937	Amyloid precursor
21	53	100.0	59	17	AAE05375	Amyloid precursor
22	53	100.0	59	19	AAW70863	Beta-amyloid precu
23	53	100.0	59	22	AAE84425	Partial sequence o
24	53	100.0	60	21	AAE69701	Beta-amyloid precu
25	53	100.0	63	18	AAE26511	Amyloid precursor
26	53	100.0	63	18	AAE26391	Amyloid precursor
27	53	100.0	63	19	AAW44747	APP-REP 751 [BAP E
28	53	100.0	63	19	AAW44746	APP-REP 751 [BAP E
29	53	100.0	63	19	AAW42975	Beta-amyloid pepti
30	53	100.0	63	19	AAW42976	Beta-amyloid pepti
31	53	100.0	67	19	AAW71377	Peptide derived fr
32	53	100.0	93	22	ABG19083	Novel human diagn
33	53	100.0	103	16	AAE74697	Beta-amyloid precu
34	53	100.0	103	19	AAE51317	Natural beta-amylo
35	53	100.0	103	20	AAE89372	Beta-amyloid pepti
36	53	100.0	103	21	AAE56103	Beta-amyloid precu
37	53	100.0	103	22	AAE12509	Beta-amyloid precu
38	53	100.0	104	19	AAE51100	Amino acid sequenc
39	53	100.0	112	17	AAE93556	Familial Alzheimer
40	53	100.0	112	20	AAE97999	London-PAD APP pol
41	53	100.0	117	19	AAE51102	Flag-amyloid prote
42	53	100.0	162	9	AAE83151	Deduced sequence 1
43	53	100.0	162	12	AAE10023	Beta-amyloid-relat
44	53	100.0	162	14	AAE37863	Deduced from clone
45	53	100.0	249	15	AAE5798	Beta-amyloid precu

ALIGNMENTS

RESULT 1

ID AAB46209 standard: peptide; 10 AA.

AC AAB46209;

DT 04-APR-2001 (first entry)

DE Human APP derived immunogenic peptide #5.

XX Amyloid deposit; APP, Abeta; brain; human; clearing response; nootropic;

KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;

KW amyloid precursor protein; Alzheimer's disease.

XX Homo sapiens.

XX WO200072880-A2.

XX 07-DEC-2000.

XX 26-MAY-2000: 2000WO-US14810.

XX 28-MAY-1999: 99US-0322289.

XX (NEUR-) NEURALAB LTD.

XX Schenk DB, Bard F, Vasquez, NJ, Yednock T;

XX WPI; 2001-032104/04.

XX Preventing or treating a disease associated with amyloid deposits,

PT especially Alzheimer's disease, comprises administering amyloid

specific antibody -

XX

PS Disclosure; Figure 19; 143bp; English.
XX
XX This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have neurotropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 53; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.00012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVKMDAEFRH 10
|||||
Db 1 EVKMDAEFRH 10
*RESULT 2
AAW70869
ID AAW70869 standard; peptide: 13 AA.
XX
XX AAW70869;
XX
XX 04-FEB-1999 (first entry)
DT
XX
XX Beta-amyloid peptide to create a monoclonal antibody.
DE
XX
XX Beta-amyloid precursor protein; beta-APP; beta-amyloid peptide;
KW antibody; amyloid deposit; Alzheimer's disease.
KM
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9844955-A1.
PN
XX
XX 15-OCT-1998.
PD
XX
XX 09-APR-1998; 98WO-US06900.
PF
XX
XX 09-APR-1997; 97US-0041850.
PR
XX
XX (MCIN/) MCINNIS P A.
PA (MIND-) MINDSET LTD.
PI
XX
XX Chain DG;
PI
XX
XX WPI; 1998-594476/50.
DR
XX
XX Preventing or inhibiting progression of Alzheimer's Disease -
PT comprises use of recombinant DNA encoding an antibody specific for
PT the N- or C-terminus of an amyloid-beta peptide
XX
XX
XX Example 1; Page 47; 58pp; English.
PS
XX
XX The present sequence represents a peptide derived from beta-amyloid
CC precursor protein (beta-APP). The peptide is a beta-amyloid
CC peptide and is used to produce a monoclonal antibody. The specification
CC describes a method for prevention or inhibition of progression of
CC Alzheimer's disease. The method comprises administering a composition
CC comprising a recombinant DNA molecule containing a gene encoding a
CC recombinant antibody end-specific for the N-terminus or the C-terminus
CC of an amyloid-beta peptide, operably linked to a promoter which is
CC expressed in the central nervous system. The recombinant antibody is

CC molecules prevent the accumulation of beta-amyloid peptides in the
CC extracellular space, interstitial fluid and cerebrospinal fluid and the
CC aggregation of such peptides into amyloid deposits in the brain. They
CC also inhibit the progression of Alzheimer's disease by inhibiting the
CC interaction of beta-amyloid peptides mediating Alzheimer's disease
CC induced neurotoxicity and inhibiting the Alzheimer's disease induced
CC complement activation and cytokine release involved in the inflammatory
CC process.
XX
SQ Sequence 13 AA;
Query Match 100.0%; Score 53; DB 19; Length 13;
Best Local Similarity 100.0%; Pred. NO. 0.00016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVKMDAEFRH 10
|||||
Db 4 EVKMDAEFRH 13
RESULT 3
AAB06315
ID AAB06315 standard; peptide: 16 AA.
XX
XX AAB06315;
XX
XX 03-OCT-2000 (first entry)
DT
XX
XX Human beta-amyloid precursor protein beta-secretase cleavage site.
DE
XX
XX Human; beta-amyloid precursor protein; beta-APP; beta-secretase;
KW subtilisin-kexin isoenzyme 1; SKI-1;
KW pro-brain-derived neurotrophic factor; PROBDNF; anti-lipemic;
KW cytotatic; vasotropic; SKI-1 inhibitor; hypercholesterolemia;
KW liver steatosis; Ras-dependent cancer; restenosis;
KW amyloid protein formation.
XX
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Cleavage-site 8..9
FT
XX
XX WO200026348-A2.
PN
XX
XX 11-MAY-2000.
PD
XX
XX 04-NOV-1999; 99WO-CA01058.
PF
XX
XX 04-NOV-1998; 98CA-2249648.
PR
XX
XX (RECL-) INST RECH CLINIQUES MONTREAL.
PA
XX
XX Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;
PI
XX
XX WPI; 2000-365601/31.
DR
XX
XX Novel soluble proteic fragment of subtilisin-kexin isoenzyme for
PT producing a polypeptide useful for treating hypercholesterolemia, liver
PT steatosis and amyloidosis, comprises a specific amino acid sequence -
XX
XX
XX Example 4; Page 51; 119pp; English.
PS
XX
XX The present sequence is the beta-secretase site of human beta-amyloid
CC precursor protein (beta-APP). The sequence may be cleaved
CC by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1
CC (SKI-1), a type-1 membrane-bound proteolase. Peptides which bind to and
CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for
CC screening inhibitors of SKI-1 activity, or for screening enhancers of
CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1
CC catalytic site may be used as inhibitors of SKI-1 activity. They may be
CC used to treat diseases involving overexpression of SKI-1 or SKI-1
CC substrate. Such diseases include hypercholesterolemia, high levels of
CC fatty acids, lipids or larnesyl pyrophosphate, liver steatosis,

CC Ras-dependent cancer, restenosis and amyloid protein formation.

XX Sequence 16 AA;

Query Match 100.0%; Score 53; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EVKMDAEFRH 10
Db 5 EVKMDAEFRH 14

RESULT 4
AAB06317 standard; peptide: 16 AA.

XX AAB06317;
XX 03-OCT-2000 (first entry)

DE Human beta-amyloid precursor protein beta-epsilon1-secretase site.

XX Human: beta-amyloid precursor protein; beta-APP;
KW beta-epsilon1-secretase; subtilisin-kexin isoenzyme 1; SKI-1;
KW pro-brain-derived neurotrophic factor; proBDNF; antilipemic;
KW cytosolic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia;
KW liver steatosis; Ras-dependent cancer; restenosis;
KW amyloid protein formation.

XX Homo sapiens.

EH Key Location/Qualifiers

FT Cleavage-site 8..9

PN WC00026348-A2.

PD 11-MAY-2000.

PF 04-NOV-1999; 99WC-CA01058.

PR 04-NOV-1998; 98CA-2249648.

XX (RECL-) INST RECH CLINIQUES MONTREAL.

XX Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

XX WPI; 2000-365601/31.

PT Novel soluble proteic fragment of subtilisin-kexin isoenzyme for
producing a polypeptide useful for treating hypercholesterolaemia, liver
steatosis and amyloidosis, comprises a specific amino acid sequence -
XX Example 4; Page 51; 119pp; English.

XX The present sequence is the beta-epsilon1-secretase site of human
beta-amyloid precursor protein (beta-APP). The sequence may be cleaved
CC by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1
CC (SKI-1), a type-1 membrane-bound proteinase. Peptides which bind to and
CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for
CC screening inhibitors of SKI-1 activity, or for screening enhancers of
CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1
CC catalytic site may be used as inhibitors of SKI-1 activity. They may be
CC used to treat diseases involving overexpression of SKI-1 or SKI-1
CC substrate. Such diseases include hypercholesterolaemia, high levels of
CC fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,
CC Ras-dependent cancer, restenosis and amyloid protein formation.

XX Sequence 16 AA;

Query Match 100.0%; Score 53; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EVKMDAEFRH 10
Db 3 EVKMDAEFRH 12

RESULT 5
AAE00608 standard; peptide: 18 AA.

XX AAE00608;
XX 02-JUL-2001 (first entry)

DE Beta-amyloid precursor protein beta-secretase cleavage site.

XX Beta-amyloid precursor protein; beta-APP; caspase; beta-secretase;
KW cysteine protease; apoptosis; caspase expression cassette; metastasis;
KW tumour; cathepsin B; urokinase; proliferation; gene therapy;
KW interdomain linker; cleavage site; Alzheimer's disease.

XX Unidentified.

XX WC0200129232-A2.

PN 26-APR-2001.

PF 19-OCT-2000; 2000WC-US28941.

PR 20-OCT-1999; 99US-0160559.

PR 14-AUG-2000; 2000US-0225564.

XX (SCIO-) SCIOS INC.

XX Corde11 B, Li Y;

XX WPI; 2001-290920/30.

PT Novel fusion polypeptide comprising first and second caspase subunit
separated by cleavage site not associated in nature with caspase
PT subunit, useful for cloning gene encoding enzymes involved in
PT proteolytic cleavage -

XX Example 2; Page 26; 116pp; English.

XX The present sequence is a beta-secretase cleavage site of beta-amyloid
CC precursor protein (beta-APP). This sequence is used to construct
CC an artificially engineered chimeric cassette comprising human caspase-3
CC with interdomain linker replaced by swedish mutant beta-secretase
CC cleavage site. This modified caspase-3 plays a pivotal role in
CC Alzheimer's disease. Caspases are a family of cysteine proteases, that
CC participate in the initiation and execution of apoptosis.
CC The present invention relates to a method for functional cloning of genes
CC encoding proteins or enzymes involved in proteolytic cleavage. The
CC invention is based on the use of caspase expression cassettes comprising
CC the coding sequence of a proteolytic cleavage site flanked by sequences
CC encoding two caspase subunits. A fusion polypeptide comprising a first
CC and a second caspase subunit, separated by a cleavage site not associated
CC in nature, is useful for cloning gene encoding enzymes involved in
CC proteolytic cleavage. An expression cassette containing fusion
CC polypeptide is used to identify a mutant cell line deficient in an
CC enzyme of interest and is also useful for diagnosis and suppression of
CC proliferation or metastases of a tumour cell characterised by
CC overexpression of a polypeptide (e.g. Cathepsin B or urokinase,
CC selectively expressed in the tumour cells). DNA encoding fusion
CC polypeptide is used in gene therapy.

XX Sequence 18 AA;

Query Match 100.0%; Score 53; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10
 |||||
 DB 7 EVKMDAEFRH 16

RESULT 6
 AAR14135

ID AAR14135 standard; peptide: 19 AA.

AC AAR14135;

DT 12-DEC-1991 (first entry)

DE Brain-derived protease substrate contg. beta-APP cleavage site.

XX Alzheimer's disease; chymase; multicatalytic protease;

KW beta-amyloid precursor protein; A4.

XX Synthetic.

OS Key Location/Qualifiers

FT Cleavage-site 4..5 /note= "chymase and multicatalytic protease site"

PN WO9113904-A.

PD 19-SEP-1991.

XX 04-MAR-1991; 91WO-US01474.

PR 05-MAR-1990; 90US-0489290.

XX (CEPH-) CEPHALON INC.

PI Siman R, Nelson RB, Kauer J, Potter H;

DR WPI: 1991-295576/40.

PT New chymotrypsin-like serine protease(s) - and their inhibitors
 are used to treat Alzheimer's disease

PS Claim 41; Page 63; 86pp; English.

XX This peptide is designed based on the sequence of beta-APP A4

CC cleavage site. Cleavage by proteases in the brain releases beta-

CC amyloid protein, the deposition of which is a feature of Alzheimer's

CC disease neuropathology. The peptide is used to screen for candidate

CC proteases which cleave between the Met and Asp residues. Two new

CC proteases have been isolated having this cleavage specificity.

CC Chymase was isolated from rat brains and multicatalytic protease was

CC isolated from human cerebral cortex. See also AAR14136-9.

XX Sequence 19 AA:

OY 1 EVKMDAEFRH 10
 |||||
 DB 1 EVKMDAEFRH 10

RESULT 7
 AAY69713

ID AAY69713 standard; peptide: 20 AA.

AC AAY69713;

DT 11-APR-2000 (first entry)

DE Beta-APP alpha-secretase substrate [KM]-APP(-10,+10).

KW Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
 KW cleavage site; beta-secretase; neurodegenerative disease;
 KW Alzheimer's disease.

OS Homo sapiens.

XX WO9964587-A1.

PD 16-DEC-1999.

PF 04-JUN-1999; 99WO-FR01326.

PR 05-JUN-1998; 98FR-0007068.

PR 31-MAR-1999; 99US-0122599.

XX (RHON) RHONE-POULENC RORER SA.

PA (UYPA-) UNIV CURIE PARIS VI P & M.

PI RhoIam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;

DR WPI: 2000-097537/08.

PT Polypeptide with beta-secretase activity, specific for wild-type

PT amyloid precursor protein, useful in treating Alzheimer's disease -

PS Example 3; Page 24; 44pp; French.

CC Peptides AAY69702-169718 represent synthetic peptide substrates for a

CC novel polypeptide with beta-secretase activity that can cleave

CC specifically the natural beta-amyloid precursor protein (bAPP). Normal

CC cleavage of the protein occurs between amino acids Met596-Asp597 and

CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel

CC polypeptide is used to identify agents that interact specifically with

CC it. These agents regulate metabolism of APP, particularly they slow down

CC or reduce production of beta-amyloid, so can be used to treat

CC neurodegenerative diseases, particularly Alzheimer's disease.

XX Sequence 20 AA:

OY 1 EVKMDAEFRH 10
 |||||
 DB 7 EVKMDAEFRH 16

RESULT 8
 AAW98002

ID AAW98002 standard; protein: 33 AA.

AC AAW98002;

DT 21-JUN-1999 (first entry)

DE Amyloid precursor protein (aa656-678) with Swedish mutation.

XX Amyloid precursor protein; APP; human; gene targeting;

KW homologous recombination; transgenic mouse; transgenic animal;

KW animal model; Alzheimer's disease.

OS Mus musculus.

XX WO9909150-A1.

PD 25-FEB-1999.

PF 18-AUG-1997; 97WO-US14507.

PR 18-AUG-1997; 97WO-US14507.

XX (FARB) BAYER CORP.

```

XX      WlraK DO;
PT      Modification of target nucleic acids - by homologous recombination,
XX      used particularly for introducing a humanised amyloid precursor
XX      protein gene into rodents for producing models of Alzheimer's
XX      disease
XX      PS      Disclosure: Page 145; 209pp; English.
XX      CC      This polypeptide comprises residues 656-678 of a murine amyloid
XX      precursor protein (APP). The invention provides a novel gene
XX      targeting strategy that facilitates the introduction of one or
XX      more specific mutations into any gene in a single double reciprocal
XX      homologous recombination step. The method has been used
XX      particularly for introducing a humanised APP gene into rodents for
XX      producing animal models of Alzheimer's disease (AD). 4 independent
XX      lines of transgenic mice (lines ES5007, ES5103, ES5401 and ES5403)
XX      have been created using the gene targeting technique applied to
XX      embryonic stem cells. In each line, the mouse APP gene was modified
XX      to encode a mouse/human hybrid (m/hAPP) where amino acid residues
XX      666-770 of APP770 were encoded by human CDNA sequences instead of
XX      mouse genomic exons (exons 16-18). Within these residues, only 3
XX      amino acid differences exist between the mouse and human proteins,
XX      i.e. Gly-676 to Arg, Phe-681 to Thr and Arg-684 to His. The
XX      exon-cDNA fusion gene therefore encodes an APP containing a
XX      humanised beta-amyloid domain. Swedish- and/or London-PAD APP
XX      mutations have also been introduced (see also AAW97997-W98001).
XX      SQ      Sequence 33 AA;
XX      Query Match 100.0%; Score 53; DB 20; Length 33;
XX      Best Local Similarity 100.0%; Pred. No. 0.00043;
XX      Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      QY      1 EVKMDAEFRH 10
XX      DB      13 EVKMDAEFRH 22
XX      RESULT 9
XX      ID      AAY69717 standard; peptide: 39 AA.
XX      AC      AAY69717;
XX      DT      11-APR-2000 (first entry)
XX      DE      Beta-APP alpha-secretase substrate [KM]-APP(-20,+20).
XX      KW      Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
XX      KW      cleavage site; beta-secretase; neurodegenerative disease;
XX      KW      Alzheimer's disease.
XX      OS      Homo sapiens.
XX      PN      MO9964587-A1.
XX      PD      16-DEC-1999.
XX      PE      04-JUN-1999; 99WO-FR01326.
XX      PR      05-JUN-1998; 98FR-0007068.
XX      PR      31-MAR-1999; 99US-0122599.
XX      PA      (RHON ) RHONE-POULENC RORER SA.
XX      PA      (UYPA-) UNIV CURIE PARIS VI P & M.
XX      PI      RhoIam M., Munoz-Gimenez N., Moutaouakil M., Cohen P., Bertrand P.
XX      DR      WPI: 2000-097337/08.

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```

XX      Polypeptide with beta-secretase activity, specific for wild-type
XX      amyloid precursor protein, useful in treating Alzheimer's disease -
XX      Example 3; Page 24; 44pp; French.
XX      PS      Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
XX      CC      novel polypeptide with beta-secretase activity that can cleave
XX      CC      specifically the natural beta-amyloid precursor protein (BAP). Normal
XX      CC      cleavage of the protein occurs between amino acids Met396 Asp597 and
XX      CC      Val636-Ile637 (positions 4-3 and 44-45 of AAY69701). The novel
XX      CC      polypeptide is used to identify agents that interact specifically with
XX      CC      it. These agents regulate metabolism of APP, particularly they slow down
XX      CC      or reduce production of beta-amyloid, so can be used to treat
XX      CC      neurodegenerative diseases, particularly Alzheimer's disease.
XX      SQ      Sequence 39 AA;
XX      Query Match 100.0%; Score 53; DB 21; Length 39;
XX      Best Local Similarity 100.0%; Pred. No. 0.00052;
XX      Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      QY      1 EVKMDAEFRH 10
XX      DB      16 EVKMDAEFRH 25
XX      RESULT 10
XX      ID      AAW26512 standard; Peptide: 45 AA.
XX      AC      AAW26512;
XX      DT      06-JAN-1998 (first entry)
XX      DE      Amyloid precursor protein fragment APP-RPP 751 (BAP del11-28).
XX      KW      Amyloid precursor protein; APP; beta-amyloid protein; BAP;
XX      KW      substrate; mutleln; secretase; Alzheimer's disease; human.
XX      OS      Chimeric Homo sapiens.
XX      OS      Chimeric synthetic.
XX      FH      Key Location/Qualifiers
XX      FT      Cleavage-site 7..8 /note= "secretase cleavage site"
XX      FT      Peptide 10..33 /label= BAP(del11-28)
XX      FT      Domain 20..42 /note= "truncated beta-amyloid protein"
XX      FT      /label= Transmembrane
XX      PN      US5656477-A.
XX      PD      12-AUG-1997.
XX      PE      01-MAY-1992; 92US-0877675.
XX      PR      20-SEP-1993; 93US-0123659.
XX      PR      01-MAY-1992; 92US-0877675.
XX      PA      (AMCY ) AMERICAN CYANAMID CO.
XX      PI      Jacobsen JS, Vitek MP;
XX      DR      WPI: 1997-414594/38.
XX      PT      Nucleic acid encoding amyloid precursor mutleln(s) - comprising
XX      PT      reporter gene and coding sequence, for identifying compounds which
XX      PT      modify the activity of proteolytic enzymes which cleave APP
XX      PS      Disclosure: Fig 5A; 84pp; English.

```

CC This peptide sequence shows the region of amyloid precursor protein
 CC (APP) that includes a truncated beta-amyloid protein (BAP) lacking
 CC the native secretase cleavage/recognition site. In an attempt to
 CC engineer an APP non-cleavable substrate for secretase, an
 CC APP-reporter (APP-REP) protein that carries the BAP deletion has
 CC been expressed in recombinant host cells. Deletion of these 18
 CC amino acids, however, still resulted in the secretion of an
 CC N-terminal APP-reporter fragment into the cytoplasm. Non-
 CC cleavable APP substrates can be used to detect other putative
 CC abnormal APP processing events. They can also be used to
 CC investigate cellular post-translational modifications to APP in
 CC order to determine the potential influence on normal secretase and
 CC abnormal BAP 'clipping' activities.

XX Sequence 45 AA:

SQ
 Query Match 100.0%; Score 53; DB 18; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0006;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
 |||||
 DB 6 EVKMDAEFRH 15

RESULT 11

AAW26392
 ID AAW26392 standard; Peptide: 45 AA.

XX AAW26392;

DT 15-DEC-1997 (first entry)

DE Amyloid precursor protein fragment APP-REP 751 (BAP del11-28).

XX Amyloid precursor protein; APP; beta-amyloid protein; BAP;

KW substrate; muteln; secretase; Alzheimer's disease; human.

XX Chimeric Homo sapiens;

OS Chimeric synthetic.

XX Key Location/Qualifiers

FT Cleavage-site 7..8 /note= "secretase cleavage site"

FT Peptide 10..33 /label= BAP(del11-28)

FT /note= "truncated beta-amyloid protein"

FT Domain 20..42

FT /label= Transmembrane

PN US5652092-A.

PD 29-JUL-1997.

PF 01-MAY-1992; 92US-0877675.

PR 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

PR 05-JUN-1995; 95US-0462859.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobsen JS, Vitek MP;

XX WPI; 1997-392937/36.

XX Screening for compounds which reduce beta-amyloid protein formation

XX - using cells which express a construct encoding a marker and an

XX amyloid precursor muteln derived from APP isoforms

XX Disclosure; Fig 5A; 84pp; English.

XX This peptide sequence shows the region of amyloid precursor protein

CC (APP) that includes a truncated beta-amyloid protein (BAP) lacking
 CC the native secretase cleavage/recognition site. In an attempt to
 CC engineer an APP non-cleavable substrate for secretase, an
 CC APP-reporter (APP-REP) protein that carries the BAP deletion has
 CC been expressed in recombinant host cells. Deletion of these 18
 CC amino acids, however, still resulted in the secretion of an
 CC N-terminal APP-reporter fragment into the cytoplasm. Non-
 CC cleavable APP substrates can be used to detect other putative
 CC abnormal APP processing events. They can also be used to
 CC investigate cellular post-translational modifications to APP in
 CC order to determine the potential influence on normal secretase and
 CC abnormal BAP 'clipping' activities.

XX Sequence 45 AA:

SQ
 Query Match 100.0%; Score 53; DB 18; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0006;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
 |||||
 DB 6 EVKMDAEFRH 15

RESULT 12

AAW4748
 ID AAW4748 standard; Protein: 45 AA.

XX AAW4748;

DT 01-JUN-1998 (first entry)

DE APP-REP 751 [BAP delta(11-28)] peptide.

XX Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;

KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;

KW Alzheimer's disease; cleavage.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Cleavage-site 7..8 /note= "putative secretase cleavage site"

FT Misc-difference 19..20 /note= "residues 11-28 of the wild type BAP sequence

FT are deleted from between these positions"

PN US5693478-A.

PD 02-DEC-1997.

PF 05-JUN-1995; 95US-0464247.

PR 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

PR 05-JUN-1995; 95US-0464247.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobsen JS, Vitek MP;

XX WPI; 1998-031744/03.

XX Amyloid precursor muteln reporter molecule assay containing antibody

XX recognisid marker - used to study pathways associated with

XX Alzheimer's disease

XX Disclosure; Fig 5A; 84pp; English.

XX This sequence represent the beta-amyloid protein sequence from the

XX construct APP-REP751 [BAP delta(11-28)]. The mutant sequence contains

XX a deletion of the wild type BAP residues 11-28. This causes a

CC shortening of the BAP sequence. This may affect cleavage of the BAP by
 CC the "secretase" dependent on whether the "secretase" recognises the
 CC cleavage site by a positional effect or by sequence. The mutant sequence
 CC can be used in a method to study secretase and beta-amyloid protein
 CC (BAP)-generating pathways associated with Alzheimer's disease by
 CC studying proteolytic cleavage of the reporter polypeptides (e.g.
 CC AAM44744 and AAM44745).

SO Sequence 45 AA;

Query Match 100.0%; Score 53; DB 19; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0006;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
 |||||
 DB 6 EVKMDAEFRH 15

RESULT 13

ID AAM42977 standard; peptide; 45 AA.

AC AAM42977;

DT 01-MAY-1998 (first entry)

DE Deletion beta-amyloid peptide (BAP) derived from APP-RP 751.

XX Beta-amyloid peptide; BAP; extracellular BAP plaque;

KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;

KM amyloid precursor protein; APP; secretase; BAP aggregation;

XX abnormal proteolytic cleavage.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain

XX 20..43

XX /note="putative transmembrane domain"

XX US5703209-A.

XX 30-DEC-1997.

XX 05-JUN-1995; 95US-0464248.

XX 20-SEP-1993; 93US-0123659.

XX 01-MAY-1992; 92US-0877675.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobson JS, Vittek MP;

XX WPI; 1998-076482/07.

XX The present sequence represents a beta-amyloid peptide (BAP), with

XX a deletion amino acids 11-28 (numbered according to AAM42976). Abnormal

XX accumulation of extracellular BAP in plaques and cerebrovascular

XX deposits is characteristic in brains of individuals suffering from

XX Alzheimer's disease and Downs syndrome. BAP is a poorly soluble,

XX self-aggregating protein which is derived from a larger amyloid precursor

XX protein (APP). APP is expressed as an integral membrane protein, and is

XX cleaved by secretase, between BAP 16lys and 17leu. Cleavage at this site

XX precludes amyloidogenesis and results in the release of the

XX amino-terminal APP fragment. Three major isoforms of APP exist: APP-695,

XX APP-751 and APP-770. These isoforms are derived by alternative splicing.

XX APP-RP 751 is a deletion construct of APP-751, which has a deletion of

XX 276 amino acids to within 15 amino acids of the BAP domain. APP can be

CC used as a substrate for studying abnormal proteolytic cleavage which
 CC results in the release of BAP, and also to screen for drugs that will
 CC inhibit such cleavage.

SO Sequence 45 AA;

Query Match 100.0%; Score 53; DB 19; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0006;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
 |||||
 DB 6 EVKMDAEFRH 15

RESULT 14

ID AAR55695 standard; Protein; 53 AA.

AC AAR55695;

DT 29-DEC-1994 (first entry)

DE Sequence of unidentified protein sequence ID number 20.

XX Amyloid precursor protein; APP; plaque; beta/A4; Alzheimers;

KW transgene; ss.

XX Synthetic.

XX WO9412627-A.

XX 09-JUN-1994.

XX 24-NOV-1993; 93WO-US11480.

XX 25-NOV-1992; 92US-0989850.

XX 09-NOV-1993; 93US-0149222.

XX (CEPH-) CEPHALON INC.

XX Howland DS, Scott RW;

XX WPI; 1994-200256/24.

XX Transgenic animal model for Alzheimer's disease - contains

XX of synapsin gene promoter

XX Example; Page 54; 94pp; English.

XX There was no apparent reference to sequence ID numbers 20, 21 or 22

XX in the specification. The specification describes a transgenic

XX animal model for Alzheimer's disease. A transgenic animal

XX harbouring a transgene coding for an amyloid protein under the

XX control of a promoter is claimed. The amyloid protein can be

XX APP695, APP751 or APP770. The coding sequence may contain a

XX mutation, including the hereditary cerebral haemorrhage with

XX amyloidosis - Dutch type (HCHWA-DT) and familial Alzheimer's

XX disease (FAD). Perhaps SO IDs 20-22 corresp. to wt, HCHWA-DT

XX and FAD?

SO Sequence 53 AA;

Query Match 100.0%; Score 53; DB 15; Length 53;
 Best Local Similarity 100.0%; Pred. No. 0.00072;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
 |||||
 DB 1 EVKMDAEFRH 10

```

RESULT 15
AAR55696
ID AAR55696 standard; Protein; 53 AA.
XX
AC AAR55696;
XX
DT 29-DEC-1994 (first entry)
XX
DE Sequence of unidentified protein sequence ID number 21.
XX
KW Amyloid precursor protein; APP; plaque; beta/A4; Alzheimers;
KM transgene; ss.
XX
OS Synthetic.
XX
PN W09412627-A.
XX
PD 09-JUN-1994.
XX
PE 24-NOV-1993; 93WO-US1480.
XX
PR 25-NOV-1992; 92US-0989850.
PR 09-NOV-1993; 93US-0149222.
XX
PA (CEPH-) CEPHALON INC.
XX
PI Howland DS, Scott RW;
XX
DR WPI: 1994-200256/24.
XX
PT Transgenic animal model for Alzheimer's disease - contains
PT transgene encoding amyloid protein under transcriptional control
PT of synapsin gene promoter
XX
PS Example: Page 54-55; 94pp; English.
XX
CC There was no apparent reference to sequence ID numbers 20, 21 or 22
CC in the specification. The specification describes a transgenic
CC animal model for Alzheimer's disease. A transgenic animal
CC harbouring a transgene coding for an amyloid protein under the
CC control of a promoter is claimed. The amyloid protein can be
CC APP695, APP751 or APP770. The coding sequence may contain a
CC mutation, including the hereditary cerebral haemorrhage with
CC amyloidosis - Dutch type (HCHWA-DT) and familial Alzheimer's
CC disease (FAD). Perhaps SQ IDs 20-22 corresp. to wt, HCHWA-DT
CC and FAD?
XX
SQ Sequence 53 AA:

Query Match 100.0%; Score 53; DB 15; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.00072;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAERRH 10
   |||||
Db 1 EVKMDAERRH 10

```

Search completed: October 29, 2002, 10:26:44
 Job time : 24.1429 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:36 ; Search time 10.4286 Seconds
(without alignments)
92.140 Million cell updates/sec

Title: US-09-580-018-5
Perfect score: 53
Sequence: 1 EVKMDAEFRH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR:71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	57	2 E60045	Alzheimer's disease
2	53	100.0	57	2 F60045	Alzheimer's disease
3	53	100.0	57	2 G60045	Alzheimer's disease
4	53	100.0	57	2 D60045	Alzheimer's disease
5	53	100.0	57	2 A60045	Alzheimer's disease
6	53	100.0	57	2 B60045	Alzheimer's disease
7	53	100.0	82	2 P00438	Alzheimer's disease
8	53	100.0	695	1 A49795	Alzheimer's disease
9	53	100.0	770	1 Q8R044	Alzheimer's disease
10	47	88.7	747	2 JH0773	Alzheimer's disease
11	46	86.8	33	2 A27485	Alzheimer's disease
12	46	86.8	695	2 S23094	Alzheimer's disease
13	46	86.8	695	2 S20550	Alzheimer's disease
14	39	73.6	142	2 E89026	Alzheimer's disease
15	38	71.7	427	2 C83591	Alzheimer's disease
16	35	60.0	402	2 S58477	Alzheimer's disease
17	35	60.0	582	2 S72637	Alzheimer's disease
18	35	66.0	774	2 A31565	Alzheimer's disease
19	35	66.0	782	2 A34219	Alzheimer's disease
20	34	64.2	442	2 P00512	Alzheimer's disease
21	34	64.2	246	2 A61140	Alzheimer's disease
22	34	64.2	400	2 S70187	Alzheimer's disease
23	34	64.2	423	2 C84991	Alzheimer's disease
24	34	64.2	647	2 T26240	Alzheimer's disease
25	34	64.2	763	2 JCA376	Alzheimer's disease
26	34	64.2	1237	2 AE1915	Alzheimer's disease
27	34	64.2	1256	2 AB2042	Alzheimer's disease
28	34	64.2	4563	1 LPHUB	Alzheimer's disease
29	33	62.3	97	1 RCBP22	Alzheimer's disease

30	33	62.3	177	2 AB3649	hypothetical prote
31	33	62.3	255	2 G90509	dolichol-phosphate
32	33	62.3	294	2 T34048	hypothetical prote
33	33	62.3	384	2 F96601	hypothetical prote
34	33	62.3	426	2 B69876	acetylornithine de
35	33	62.3	626	2 AF0358	conserved hypothet
36	33	62.3	912	2 H71931	hypothetical prote
37	33	62.3	927	2 T38127	phosphoprotein - f
38	33	62.3	1265	2 T51498	hypothetical prote
39	33	62.3	1579	2 S59801	protein kinase SSK
40	33	62.3	1906	2 AD2443	hypothetical prote
41	32	60.4	113	2 AH0923	conserved hypothet
42	32	60.4	132	2 JQ0737	RnpA protein - Mic
43	32	60.4	173	2 G64318	hypothetical prote
44	32	60.4	319	2 S76960	hypothetical prote
45	32	60.4	350	2 G75421	probable serine/ch

ALIGNMENTS

RESULT 1
E60045 Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C:Species: Ovis sp. (sheep)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: E60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-References: EMBL:X56130
C:Superfamily: Alzheimer's disease amyloid beta protein; animal knitz-type protein
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 53; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
Db 2 EVKMDAEFRH 11

RESULT 2

F60045 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: F60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-References: EMBL:X56127; NID:q1895; PIDN:CAA39592.1; PID:q1896
C:Superfamily: Alzheimer's disease amyloid beta protein; animal knitz-type protein
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 53; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
Db 2 EVKMDAEFRH 11

```
RESULT 3
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      100.0%; Score 53; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
    |||||||||
Db 2 EVKMDAEFRH 11

RESULT 4
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: D60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56124
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      100.0%; Score 53; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
    |||||||||
Db 2 EVKMDAEFRH 11

RESULT 5
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      100.0%; Score 53; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
    |||||||||
Db 2 EVKMDAEFRH 11

RESULT 6
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56128; NID:92165; PIDN:CA939593.1; PID:92166
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      100.0%; Score 53; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
    |||||||||
Db 2 EVKMDAEFRH 11

RESULT 7
P00438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: P00438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
A:Reference number: P00438; MUID:93075180
A:Accession: P00438
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:M83558; GB:M83657
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match      100.0%; Score 53; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0008;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
    |||||||||
Db 13 EVKMDAEFRH 22

RESULT 8
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlisky, M.B.; Tolian, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
```


A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a
A:Reference number: A49795; MUID:91273117
A:Accession: A49795
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <PDD>
A:Cross-references: GB:M58727; NID:9342062; PIDN:AAA36829.1; PID:9342063
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing

Query Match 100.0%; Score 53; DB 1; Length 695;
Best local similarity 100.0%; Pred. No. 0.0089;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
|||||
Db 593 EVKMDAEFRH 602

RESULT 9
ORF004
Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibi
N:Contents: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence revision 28-Jul-1995 #text change 15-Sep-2000
A:Accession: S02260; S05194; A32277; A32486; I39452; I39451; I59562; A44
4668; A28583; A29302; A60805; J10082; S06121; A60355; A59011; A33984; S29076; S38252; S3
Nucleic Acids Res. 17, 517-522, 1989
A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A:Reference number: S02260; MUID:89128427
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288, 'V', 365-770 <LEM1>
A:Cross-references: EMBL:X13466
A>Note: alternative splice form APP(695)
R:Lemaire, H.G.
Submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
A:Cross-references: EMBL:X13466; NID:935598; PIDN:CAA31830.1; PID:9871360
A>Note: alternative splice form APP(695)
R:La Pauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A:Reference number: A32277; MUID:89165870
A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LAF>
A:Cross-references: GB:M24546; GB:M24547; NID:9341102; PIDN:AA313654.1; PID:9516074
R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A:Reference number: A33260; MUID:89392030
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JOH>
A:Cross-references: GB:M29270; NID:9178863; PIDN:AAA51768.1; PID:9178865
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A:Reference number: A35486; MUID:90321244
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PRE1>
A>Note: 693-Gln was found in DNA isolated from HCWA-D patients
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.

A:Reference number: I39451; MUID:90236318
A:Accession: I39452
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-770 <YOS1>
A:Cross-references: GB:M3112; NID:9178613; PIDN:AAB59502.1; PID:9178616
A:Accession: I39451
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-530, 'QMLMPVIPAWEAKVR' <YOS2>
A:Cross-references: GB:M34875; NID:9178608; PIDN:AAB59501.1; PID:9178615
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168
A:Contents: annotation; erratum
A>Note: revised physical map for reference I39451
R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du
Science 248, 1124-1126, 1990
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo
A:Reference number: I39453; MUID:90260663
A:Accession: I39453
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LEV>
A:Cross-references: GB:M37896; NID:9178618; PIDN:AAA51727.1; PID:9178620
A>Note: a mutation with 693-Gln is presented
R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe
A:Reference number: I59562; MUID:92022553
A:Accession: I59562
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: GB:S57665; NID:9236720; PIDN:AAB19991.1; PID:9236721
R:Kamino, K.; Orr, H.T.; Payant, H.; Wilsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anders
drakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Mart
Am. J. Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t
A:Reference number: A44017; MUID:93035397
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <KAM1>
A:Cross-references: GB:S45135; NID:9257377; PIDN:AAB33645.1; PID:9257378
A:Experimental source: familial Alzheimer disease family SB
A>Note: sequence extracted from NCBI backbone (NCBI:P.115374)
A:Accession: B44017
A:Molecule type: DNA
A:Residues: 687-718 <KAM2>
A:Cross-references: GB:S45136; NID:9257379; PIDN:AAB33646.1; PID:9257380
A:Experimental source: familial Alzheimer disease family LIT
A>Note: sequence extracted from NCBI backbone (NCBI:P.115376)
A:Title: this sequence has a silent mutation
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.
Nature 325, 733-736, 1987
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-sur
A:Reference number: A03134; MUID:87144572
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: GB:I00264; NID:928525; PIDN:CAA6374.1; PID:928526
A>Note: alternative splice form APP(695)
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascula
A:Reference number: A29030; MUID:87231971
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: GB:M16765; NID:9178539; PIDN:AAA51722.1; PID:9178540
A>Note: the authors translated the codon GAG for residue 647 as Asp
R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Salafioti, U.; Gajdusek, D.C.
Science 255, 877-880, 1987

A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
 A:Reference number: A47584; MUID:87120328
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756, 'S', 758-770 <GOL>
 A:Cross-references: GB:M1553; NID:g178706; PIDN:AAA35540.1; PID:g178707
 A:Experimental source: brain
 R:Tanzil, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
 Science 235, 880-884, 1987
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
 A:Reference number: A47585; MUID:87120329
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TAN1>
 A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
 R:Dyrks, T.; Weidemann, A.; Muthaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
 EMBO J. 7, 949-957, 1988
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
 A:Reference number: S02638; MUID:88296437
 A:Accession: S02638
 A:Molecule type: mRNA
 A:Residues: 672-678 <DYR>
 R:Tanzil, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Newe
 Nature 331, 528-530, 1988
 A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
 A:Reference number: S00707; MUID:88122640
 A:Accession: S00707
 A:Molecule type: mRNA
 A:Residues: 286-344, 'I', 365-366 <TAN2>
 A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
 A:Experimental source: promyelocytic leukemia cell line HL60
 A:Note: alternative splice form APP(751)
 R:Porte, P.; Gonzalez-Del-Hita, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
 Nature 331, 525-527, 1988
 A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
 A:Reference number: S00925; MUID:88122639
 A:Accession: S00925
 A:Molecule type: mRNA
 A:Residues: 1-344, 'I', 365-770 <PO2>
 A:Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
 A:Note: alternative splice form APP(751)
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shioiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibit
 A:Reference number: A38949; MUID:88122641
 A:Accession: A38949
 A:Molecule type: mRNA
 A:Residues: 287-367 <KIT>
 A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
 A:Experimental source: glioblastoma cell line
 A:Note: alternative splice form APP(770)
 R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
 Brain Res. Mol. Brain Res. 4, 121-131, 1998
 A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three F
 A:Reference number: A30320
 A:Accession: A30320
 A:Molecule type: mRNA
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-770 <VIT1>
 A:Accession: B30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 122-288, 'V', 365-770 <VIT2>
 A:Accession: C30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 606-770 <VIT3>
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
 A:Reference number: A31087; MUID:88124954
 A:Accession: A31087
 A:Molecule type: mRNA

A:Residues: 507-770 <A1>
 A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
 A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue
 8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue
 A:Note: the cited Genbank accession number, J03594, is not in release 101.0
 R:Maisters, C.L.; Muthaup, G.; Simms, G.; Pottinger, J.; Martins, R.N.; Beyreuther,
 Query Match 100.0%; Score 53; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVKMDAEFRH 10
 Db 668 EVKMDAEFRH 677
 RESULT 10
 JH0773
 Alzheimer's disease amyloid beta protein precursor - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
 C:Accession: JH0773
 R:Okado, H.; Okamoto, H.
 Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
 A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: development
 A:Reference number: JH0773; MUID:93129227
 A:Accession: JH0773
 A:Molecule type: mRNA
 A:Residues: 1-747 <OKA>
 A:Cross-references: GB:S52417; NID:g263150; PIDN:AA24853.1; PID:g263151
 A:Experimental source: larva
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
 C:Keywords: alternative splicing; amyloid
 F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 Query Match 88.7%; Score 47; DB 2; Length 747;
 Best Local Similarity 80.0%; Pred. No. 0.17;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVKMDAEFRH 10
 Db 645 EVKMDSEYRH 654
 RESULT 11
 S23094
 beta-amyloid protein precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
 C:Accession: S23094
 R:Kojima, S.; Omori, M.
 FEBS Lett. 304, 57-60, 1992
 A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic protein
 A:Reference number: S23094; MUID:92316198
 A:Accession: S23094
 A:Molecule type: protein
 A:Residues: 1-33 <KOJ>
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
 Query Match 86.8%; Score 46; DB 2; Length 33;
 Best Local Similarity 90.0%; Pred. No. 0.008;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EVKMDAEFRH 10
 Db 2 EVKMDAEFRH 11
 RESULT 12
 A27485
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
 N:Alternate names: proteinase nexin II
 C:Species: Mus musculus (house mouse)

C>Date: 31-Mar-1989 #sequence-revision 31-Mar-1989 #text-change 13-Aug-1999
 C:Accession: A27485; S19727; 149485
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor
 A:Reference number: A27485; MUID:8106489
 A:Accession: A27485
 A:Molecule type: mRNA
 A:Residues: 1-695 <YAM>
 A:Cross-References: GB:M18373; NID:9191568; PIDN:AAA37139.1; PID:9309085
 A:Experimental source: brain
 R:de Strooper, B.; van Leuven, F.; van den Bergh, H.
 Biochem. Biophys. Acta 1129, 141-143, 1991
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
 A:Reference number: S19727; MUID:92096458
 A:Accession: S19727
 A:Molecule type: mRNA
 A:Residues: 1-210; 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
 A:Cross-References: EMBL:X59379
 R:Izumi, R.; Yamada, T.; Yoshikawa, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
 Gene 112, 189-195, 1992
 A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's
 A:Reference number: I49485; MUID:92209998
 A:Accession: I49485
 A:Status: translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-19 <RES>
 A:Cross-References: GB:D10603; NID:9220328; PIDN:BA01456.1; PID:9220329
 C:Genetics:
 A:Map position: 16c3
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Knutlz-type proteinase I
 C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 86.8%; Score 46; DB 2; Length 695;
 Best Local Similarity 90.0%; Pred. No. 0.25; 1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKMDAEPFH 10
 Db 593 EYKMDAEPFH 602

RESULT 13
 S00550
 Alzheimer's disease amyloid beta protein precursor - rat
 N:Alternate names: beta-A4 amyloid protein
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Jun-1989 #sequence-revision 30-Jun-1989 #text-change 13-Aug-1999
 C:Accession: S00550; A41245; A39820; S46251
 R:Shivers, B.D.; Hlilich, C.; Mulhapp, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
 EMBO J. 7, 1365-1370, 1988
 A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
 A:Reference number: S00550; MUID:88312583
 A:Accession: S00550
 A:Molecule type: mRNA
 A:Residues: 1-695 <SHI>
 A:Cross-References: EMBL:X07648; NID:955616; PIDN:CAA30488.1; PID:955617
 R:Schubert, D.; Schröder, R.; Lacobiere, M.; Salton, T.; Cole, G.
 Science 241, 223-226, 1988
 A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
 A:Reference number: A41245; MUID:88264430
 A:Accession: A41245
 A:Molecule type: protein
 A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
 A:Note: evidence for heparan sulfate attachment
 R:Hesse, L.; Behr, D.; Masters, C.L.; Mulhapp, G.
 FEBS Lett. 349, 109-116, 1994
 A:Title: The beta-A4 amyloid precursor protein binding to copper.
 A:Reference number: S46251; MUID:94320627
 A:Contents: annotation; copper binding sites
 A:Note: rat peptides were isolated but not sequenced
 R:Potempa, A.; Styles, J.; Menta, P.; Kim, K.S.; Miller, D.L.
 J. Biol. Chem. 266, 8464-8469, 1991

A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat b
 A:Reference number: A39820; MUID:91217087
 A:Accession: A39820
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 18-32 <POT>
 A:Experimental source: brain
 C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Knutlz-type proteinase
 C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
 F:625-648/Domain: transmembrane #status predicted <YMM>

Query Match 86.8%; Score 46; DB 2; Length 695;
 Best Local Similarity 90.0%; Pred. No. 0.25;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKMDAEPFH 10
 Db 593 EYKMDAEPFH 602

RESULT 14
 E89026
 protein F13A2.1 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 10-May-2001 #sequence-revision 10-May-2001 #text-change 10-May-2001
 A:Accession: E89026
 R:Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
 A:Accession: E89026
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-142 <STO>
 A:Cross-References: GB:chr_V; PIDN:AAB69895.1; PID:92384795; GSPDB:GN00023; CESP:F13A
 C:Genetics:
 A:Gene: F13A2.1
 A:Map position: 5

Query Match 73.6%; Score 39; DB 2; Length 142;
 Best Local Similarity 77.8%; Pred. No. 1.1;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKMDAEPFH 9
 Db 56 EYKMDAEPFH 64

RESULT 15
 C83591
 N-carbamoyl-beta-alanine amidohydrolyase PA0444 [imported] - Pseudomonas aeruginosa (s
 C:Species: Pseudomonas aeruginosa
 C>Date: 15-Sep-2000 #sequence-revision 15-Sep-2000 #text-change 31-Dec-2000
 C:Accession: C83591
 R:Stover, C.K.; Pham, X.Q.; Errin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.;
 Adman, S.; Yan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lathig, K.; L
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
 A:Reference number: A82950; MUID:20437337
 A:Accession: C83591
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-427 <STO>
 A:Cross-References: GB:AE004481; GB:AE004091; NID:99946293; PIDN:AA003833.1; GSPDB:GN
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA0444
 C:Superfamily: N-carbamyl-L-amino acid amidohydrolyase

Query Match 71.78; Score 38; DB 2; Length 427;
Best Local Similarity 70.08; Pred. No. 6.4;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EYKMDAFFFFR 10
|||:|||
Db 289 EYKMTLDFRR 298

Search completed: October 29, 2002, 10:31:02
Job time : 11.4286 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:36 ; Search time 5 seconds
(without alignments)
77.439 Million cell updates/sec

Title: US-09-580-018-5
Perfect score: 53
Sequence: 1 EVKMAEFRR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	57	1 A4_PIG	Q29023 sus scrofa
2	53	100.0	57	1 A4_URSLA	Q29149 ursus marit
3	53	100.0	58	1 A4_CANFA	Q28280 canis famill
4	53	100.0	58	1 A4_RABIT	Q28748 oryctolagus
5	53	100.0	58	1 A4_SHEEP	Q28757 ovis aries
6	53	100.0	59	1 A4_BOVIN	Q28053 bos taurus
7	53	100.0	751	1 A4_SALSC	Q95241 salmtr sci
8	53	100.0	770	1 A4_HUMAN	P05067 homo sapien
9	46	86.8	770	1 A4_MOUSE	P12023 mus musculu
10	46	86.8	770	1 A4_RAT	P08582 rattus norv
11	35	66.0	402	1 R0S1_SCHPO	P53693 schizosacch
12	35	66.0	782	1 BICD_DROME	P16568 drosophila
13	34	64.2	269	1 T2S1_STRFI	O52512 streptomyce
14	34	64.2	394	1 EFTU_BUCAI	O31297 buchnera ap
15	34	64.2	4563	1 APB_HUMAN	P04114 homo sapien
16	33	62.3	97	1 ABC2_BPR22	P11191 bacterioph
17	33	62.3	927	1 CC15_SCHPO	O09892 schizosacch
18	33	62.3	1579	1 SSK2_YEAST	P53599 saccharomyc
19	32	60.4	132	1 RNP4_MICDU	P21172 micrococcc
20	32	60.4	173	1 Y150_MENJA	O57614 methanococc
21	32	60.4	354	1 BCPA_CHLIT	O46195 chlorobium
22	32	60.4	365	1 BCPA_CHLIT	O46393 chlorobium
23	32	60.4	502	1 YGCL_ECOLI	O46901 escherichia
24	32	60.4	780	1 K6PL_HUMAN	P17858 homo sapien
25	31	58.5	198	1 TNE4_MOUSE	P43488 mus musculu
26	31	58.5	323	1 DHBX_MOUSE	P70694 mus musculu
27	31	58.5	323	1 PEZR_RABIT	P80508 oryctolagus
28	31	58.5	351	1 VA0D_HUMAN	P12953 homo sapien
29	31	58.5	351	1 VA0D_MOUSE	P51863 mus musculu
30	31	58.5	478	1 G6PD_BORBU	O51581 borrelia bu
31	31	58.5	479	1 Y098_MYCPN	P75535 mycoplasma
32	31	58.5	757	1 ECR_LUCGU	O18531 lucilia cup
33	31	58.5	1451	1 A2M2_MOUSE	P28666 mus musculu

34	31	58.5	1476	1 A2M1_MOUSE	P28665 mus musculu
35	31	58.5	1477	1 A1I3_RAT	P14046 rattus norv
36	31	58.5	3562	1 PGCV_CHICK	O90953 gallus gall
37	31	58.5	4644	1 DYHC_MOUSE	O91hu4 mus musculu
38	31	58.5	4644	1 DYHC_RAT	P38650 rattus norv
39	31	58.5	376	1 AROC_YEAST	P28777 saccharomyc
40	30	56.6	78	1 RL31_RICCN	O924d0 rickettsia
41	30	56.6	78	1 RL31_RICPR	O92e47 rickettsia
42	30	56.6	177	1 BLC_CITER	O46036 citrobacter
43	30	56.6	177	1 BLC_ECOLI	P39281 escherichia
44	30	56.6	193	1 YEXN_AERSA	P45785 aeromonas s
45	30	56.6	197	1 OM26_HAEIN	O57483 haemophilus

ALIGNMENTS

RESULT 1

A4_PIG STANDARD: PRT: 57 AA.

AC Q29023;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
protein (beta-Ap) (A-beta)] (Fragment).
OS App.
GN Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain.
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).

- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
G(O) (BY SIMILARITY).
CC - SUBCELLULAR LOCATION: Type I membrane protein.
CC - SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL: X56127; CAA39592.1; -
CC HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 48
FT CHAIN 6 48
FT DOWNIN <1 33
FT TRANSM 34 57
FT NON_TER 57 57
FT SEQUENCE 57 AA; 6172 MW; 84209DB8EBA82DFA CRC64;

Query Match 100.0%; Score 53; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00046;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMAEFRR 10
|||||||

```

Db      2  EVKMDAEFRH 11

RESULT 2
A4_URSWA  STANDARD:  PRT:  57 AA.
ID  A4_URSWA  029149;
AC  029149;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  30-MAY-2000 (Rel. 39, Last annotation update)
DE  Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE  protein (Beta-Ap4) (A-beta)] (Fragment).
GN  A4.
OS  Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX  NCBI_TaxID=29073;
[1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Brain;
RX  MEDLINE=92017079; PubMed=1656157;
RA  Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT  "Conservation of the sequence of the Alzheimer's disease amyloid
RT  peptide in dog, polar bear and five other mammals by cross-species
RT  polymerase chain reaction analysis.";
RL  Brain Res. Mol. Brain Res. 10:299-305(1991).
CC  -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC  INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC  G(O) (BY SIMILARITY).
CC  -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC  or send an email to license@isb-sib.ch).
-----
DR  EMBL: X56128; CAA39593.1; -.
DR  HSSP: P05067; 1BA4.
DR  InterPro: IPR001868; A4_APP.
DR  PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR  PROSITE: PS00320; A4_INTRA; PARTIAL.
KW  Glycoprotein; Amyloid; Neurone; Transmembrane.
FT  NON_TER 1
FT  CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT  DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 34 57 POTENTIAL.
FT  NON_TER 57
SQ  SEQUENCE 57 AA; 6172 MW; 84209D88BA82DFA CRC64;

Query Match 100.0%; Score 53; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1  EVKMDAEFRH 10
Db 2  EVKMDAEFRH 11

RESULT 3
A4_CANFA  STANDARD:  PRT:  58 AA.
ID  A4_CANFA  028280;
AC  028280;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  30-MAY-2000 (Rel. 39, Last annotation update)
DE  Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE  protein (Beta-Ap4) (A-beta)] (Fragment).
GN  A4.
OS  Canis familiaris (Dog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX  NCBI_TaxID=9615;
[1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Kidney;
RX  MEDLINE=92017079; PubMed=1656157;
RA  Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT  "Conservation of the sequence of the Alzheimer's disease amyloid
RT  peptide in dog, polar bear and five other mammals by cross-species
RT  polymerase chain reaction analysis.";
RL  Brain Res. Mol. Brain Res. 10:299-305(1991).
CC  -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC  INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC  G(O) (BY SIMILARITY).
CC  -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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-----
DR  EMBL: X56125; CAA39590.1; -.
DR  HSSP: P05067; 1BA4.
DR  InterPro: IPR001868; A4_APP.
DR  PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR  PROSITE: PS00320; A4_INTRA; PARTIAL.
KW  Glycoprotein; Amyloid; Neurone; Transmembrane.
FT  NON_TER 1
FT  CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT  DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 35 58 POTENTIAL.
FT  NON_TER 58
SQ  SEQUENCE 58 AA; 6285 MW; 8469D489A2E12DFA CRC64;

Query Match 100.0%; Score 53; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1  EVKMDAEFRH 10
Db 3  EVKMDAEFRH 12

RESULT 4
A4_RABIT  STANDARD:  PRT:  58 AA.
ID  A4_RABIT  028748;
AC  028748;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE  protein (Beta-Ap4) (A-beta)] (Fragment).
GN  A4.
OS  Oryctolagus cuniculus (Rabbit).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX  NCBI_TaxID=9986;
[1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Brain;
RX  MEDLINE=92017079; PubMed=1656157;
RA  Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT  "Conservation of the sequence of the Alzheimer's disease amyloid
RT  peptide in dog, polar bear and five other mammals by cross-species
RT  polymerase chain reaction analysis.";
RL  Brain Res. Mol. Brain Res. 10:299-305(1991).
CC  -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC  INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

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CC G(O) (BY SIMILARITY).
CC SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC -----
DR EMBL: X56129; CAA39594.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 53; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEFRH 10
Db 2 EVKMDAEFRH 11

RESULT 5
A4_SHEEP STANDARD; PRT; 58 AA.
ID A4_SHEEP
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [contains: Beta-amyloid
DE protein (Beta-Ap) (A-beta)] (Fragment).
GN APP.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RA "Conservation of the sequence of the Alzheimer's disease amyloid
RA peptide in dog, polar bear and five other mammals by cross-species
RA polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
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DR EMBL: X56130; CAA39595.1; -.
DR HSSP: P05067; 1AHL.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 53; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEFRH 10
Db 2 EVKMDAEFRH 11

RESULT 6
A4_BOVIN STANDARD; PRT; 59 AA.
ID A4_BOVIN
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [contains: Beta-amyloid
DE protein (Beta-Ap) (A-beta)] (Fragment).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RA "Conservation of the sequence of the Alzheimer's disease amyloid
RA peptide in dog, polar bear and five other mammals by cross-species
RA polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC -----
DR EMBL: X56124; CAA39589.1; -.
DR EMBL: X56126; CAA39591.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 35 58 POTENTIAL.
FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
FT
```

FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;
Query Match 100.0%; Score 53; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. NO. 0.00048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVKMDAEFRH 10
| | | | | | | | | |
Db 3 EVKMDAEFRH 12
RESULT 7
A4_SAISC STANDARD: PRT; 751 AA.
ID A4_SAISC
AC Q95241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-amyloid protein (beta-ApP) (A-beta)].
GN App.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver, and Kidney;
MEDLINE=96108492; PubMed=8532114;
RT Levy E., Anorim A., Frangione B., Walker L.C.;
"Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy";
RL Neurobiol. Aging 16:805-808(1995).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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CC -----
DR EMBL: S81024; AADI347.1; -.
DR HSSP: P05067; 1AAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
FT SIGNAL: 1 Serine protease inhibitor.
FT SIGNAL 17 BY SIMILARITY.
FT CHAIN 18 751 A4 PROTEIN.
FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN 18 680
FT TRANSMEM 681 704
FT DOMAIN 705 751
FT DOMAIN 287 345
FT SITE 740 743
FT ACT_SITE 301 302
FT DISULFID 291 341
FT DISULFID 300 324
FT DISULFID 316 337
FT CARBOHYD 523 523
FT CARBOHYD 552 552
SQ SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;
Query Match 100.0%; Score 53; DB 1; Length 751;
Best Local Similarity 100.0%; Pred. NO. 0.0066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVKMDAEFRH 10
| | | | | | | | | |
Db 649 EVKMDAEFRH 658
RESULT 8
A4_HUMAN STANDARD: PRT; 770 AA.
ID A4_HUMAN
AC P05067; P09000; Q16011;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II) (PN-II) (APP) [Contains: Beta-amyloid protein (beta-ApP) (A-beta)].
GN APP OR A4 OR CVA4 OR ADL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
MEDLINE=87144572; PubMed=2881207;
RT Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grieschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
"The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor";
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88122639; PubMed=2893289;
RT Ponte P., Gonzalez-Dewhilt P., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;
"A new A4 amyloid mRNA contains a domain homologous to serine protease inhibitors";
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89128427; PubMed=2783775;
RT Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayne R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.;
"The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons";
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97263807; PubMed=9108164;
RT Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M., Saito M., Tsukuni S., Sakaki Y.;
"A novel method for making nested deletions and its application for sequencing of a 300 kb region of human APP locus";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [5]
RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;

RA Tanzi R.E., McClatchey A.I., Lampertl E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
RL Nature 331:528-530(1988).
RN [6]
RX MEDLINE=287-367 FROM N.A.
RA MEDLINE=88122641; PubMed=2893291;
RA Kikuchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
RN [7]
RX MEDLINE=284-289 AND 365-770 FROM N.A.
RA MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [8]
RX MEDLINE=507-770 FROM N.A.
RA MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [9]
RX MEDLINE=672-681.
RA MEDLINE=88035004; PubMed=3312495;
RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
RA Tountellotte W.W., Huebner V., Shively J.E.;
RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
RT and partial sequence of a 4,200-dalton peptide isolated from cortical
RT microvessels.";
RL J. Neurochem. 49:1394-1401(1987).
RN [10]
RX MEDLINE=739-770 FROM N.A.
RA MEDLINE=90236318; PubMed=2110105;
RA Yoshikaki S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";
RL Gene 87:257-263(1990).
RN [11]
RX MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [12]
RX MEDLINE=18-50.
RA MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
RN [13]
RX MEDLINE=89384866; PubMed=2506449;
RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
RA Sinha S.;
RT "The secreted form of the Alzheimer's amyloid precursor protein with
RT the Kunitz domain is protease nexin-II.";
RL Nature 341:144-147(1989).
RN [14]
RX MEDLINE=90211252; PubMed=1969731;
RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
RT disease amyloid protein precursor.";

RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
RN [15]
RX COMPLEX WITH G(O).
RA MEDLINE=93188965; PubMed=8446172;
RA Nishimoto I., Okamoto T., Matsura Y., Takahashi S., Okamoto T.,
RA Murayama Y., Ogata E.;
RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
RT protein G(O).";
RL Nature 362:75-79(1993).
RN [16]
RX X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
RA MEDLINE=99215582; PubMed=10201399;
RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinstry W.J.,
RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
RA Parker M.W.;
RT "Crystal structure of the N-terminal, growth factor-like domain of
RT Alzheimer amyloid precursor protein.";
RL Nat. Struct. Biol. 6:327-331(1999).
RN [17]
RX X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
RA MEDLINE=91104913; PubMed=2125487;
RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kosiakof A.A.;
RT "X-ray crystal structure of the protease inhibitor domain of
RT Alzheimer's amyloid beta-protein precursor.";
RL Biochemistry 29:10018-10022(1990).
RN [18]
RX STRUCTURE BY NMR OF 289-344.
RA MEDLINE=92031488; PubMed=1718421;
RA Heald S.L., Tilton R.F., Jr., Hammond L.S., Lee A., Bayney R.M.,
RA Kmarak M.E., Ramahdran T.V., Dreyer R.N., Davis G., Untereck A.,
RA Tamburini P.P.;
RT "Sequential NMR resonance assignment and structure determination of
RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
RT precursor protein.";
RL Biochemistry 30:10467-10478(1991).
RN [19]
RX STRUCTURE BY NMR OF 672-699.
RA MEDLINE=94281210; PubMed=7516706;
RA Talafoos J., Marchowski K.J., Klopman G., Zagorski M.G.;
RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
RL Biochemistry 33:7788-7796(1994).
RN [20]
RX STRUCTURE BY NMR OF 696-706.
RA MEDLINE=97128622; PubMed=8973180;
RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
RT membrane-mimicking environment.";
RL Biochemistry 35:16094-16104(1996).
RN [21]
RX STRUCTURE BY NMR OF 672-711.
RA MEDLINE=98359783; PubMed=9693002;
RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscible
RT environment. Is the membrane-spanning domain where we think it is?";
RL Biochemistry 37:11064-11077(1998).
RN [22]
RX STRUCTURE BY NMR OF 672-699.
RA MEDLINE=20400066; PubMed=10940222;
RA Poulsen S.-A., Watson A.A., Craik D.J.;
RT "Solution structures in aqueous SDS micelles of two amyloid beta
RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
RT site.";
RL J. Struct. Biol. 130:142-152(2000).
RN [23]
RX STRUCTURE BY NMR OF 681-706.
RA MEDLINE=20400065; PubMed=10940221;
RA Zhang S., Iwata K., Lachenmann M.J., Peng J.W., Li S., Stimson E.R.,
RA Lu Y., Felix A.M., Maggioni J.E., Lee J.P.;
RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in
RT water.";
RL J. Struct. Biol. 130:130-141(2000).
RN [24]
RX SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.

RA MEDLINE=88296437; PubMed=2900137;
RA Dyrys T., Weitemann A., Muthaup G., Salbaum J.M., Lemaire H.-G.,
RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
RT "Identification, transmembrane orientation and biogenesis of the
RT amyloid A4 precursor of Alzheimer's disease.";
Query Match 100.0%; Score 53; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 EVKMDAEFRH 10
Db 668 EVKMDAEFRH 677
RESULT 9
A4_MOUSE STANDARD; PRT; 770 AA.
AC P12023;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (AG).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC STRAIN-BALB/C; TISSUE-Brain;
RA MEDLINE=92096458; PubMed=1756177;
RT de Strooper B., van Leuven F., van den Bergh H.;
RT "The amyloid beta protein precursor or proteinase nexin II from mouse
RT is closer related to its human homolog than previously reported.";
RL Biochim. Biophys. Acta 1129:141-143(1991).
RN [2]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE-Brain;
RA MEDLINE=88106489; PubMed=3322280;
RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sasaki Y.;
RT "Complementary DNA for the mouse homolog of the human amyloid beta
RT protein precursor.";
RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN [3]
RP REVISIONS.
RA Yamada T.;
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 289-364 FROM N.A.
RC STRAIN-CD-1; TISSUE-Placenta;
RA MEDLINE=89345111; PubMed=2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RT precursor of Mus domestica.";
RL Nucleic Acids Res. 17:5396-5396(1989).
RN [5]
RP SEQUENCE OF 1-19 FROM N.A.
RC MEDLINE=92209998; PubMed=1555768;
RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA Sakai Y.;
RT "Positive and negative regulatory elements for the expression of the
RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL Gene 112:189-195(1992).
RN [6]
RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE-Brain, and Kidney;
RA MEDLINE=89149813; PubMed=2493250;
RA Yamada T., Sasaki H., Dohura K., Goto I., Sasaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RT for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor.";

RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
CC LIVER.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.

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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; X59379; -; NOT_ANNOTATED_CDS.
CC EMBL; M18373; AAA37139.1; -;
CC EMBL; X15210; CAA33280.1; -;
CC EMBL; D10603; BAA01456.1; -;
CC EMBL; M24397; AAA39929.1; -;
CC PIR; A27485; A27485.
CC PIR; S04855; S04855.
CC PIR; S19727; S19727.
CC HSSP; P05067; IQCM.
CC MGD; MGI:88059; APP.
CC InterPro; IPR001868; A4_APP.
CC InterPro; IPR002223; Kunitz_BPTI.
CC Pfam; PF02177; A4_EXTRA; 1.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC PRINTS; PR00203; AMYLOIDA4.
CC PRINTS; PR00759; BASICPTASE.
CC SMART; SM00006; A4_EXTRA; 1.
CC SMART; SM00131; KU; 1.
CC PROSITE; PS00319; A4_EXTRA; 1.
CC PROSITE; PS00320; A4_INTRA; 1.
CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.
CC PROSITE; PS50279; BPTI_KUNITZ_2; 1.
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
CC KW Alternative splicing; Serine protease inhibitor.
CC SIGNAL 1 17
CC CHAIN 18 770
FT FT
FT DOMAIN 18 699
FT TRANSSEM 700 723
FT DOMAIN 724 770
FT DOMAIN 673 715
FT DOMAIN 287 345
FT SITE 759 762
FT DISULFID 291 341
FT DISULFID 300 324
FT DISULFID 316 337
FT CARBOHYD 542 542
FT CARBOHYD 571 571
FT CARBOHYD 571 571
FT VARSPLIC 289 289
FT VARSPLIC 290 364
FT VARSPLIC 346 380
SO SEQUENCE 770 AA; 86752 MW; 26C50DE0890CA7A CRC64;
Query Match 86.8%; Score 46; DB 1; Length 770;
Best Local Similarity 90.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 EVKMDAEFRH 10
|||||||

DB 668 EVKMDAEFGH 677

RESULT 10

ID A4_RAT STANDARD: PRT: 770 AA.

AC P08592;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog precursor (Amyloidogenic glycoprotein) (Ag).

DE (Amyloidogenic glycoprotein) (Ag).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxId=10116;

OX NCBI

RN [1]

RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=89183625; PubMed=2648331;

RT Kang J., Mueller-Hill B.;

RT "The sequence of the two extra exons in rat preA4.";

RL Nucleic Acids Res. 17:2130-2130(1989).

CC -1- SUPRACELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695), APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.

CC -----

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CC -----

DR EMBL: X07648; CAA30488.1; -

DR EMBL: X14066; CAA32229.1; -

DR PIR: S00550; S00550.

DR PIR: S03607; S03607.

DR HSSP: P05067; IAAP.

DR InterPro: IPR001868; A4_APP.

DR InterPro: IPR002223; Kunitz_BPTI.

DR Pfam: PF02177; A4_EXTRA; 1.

DR Pfam: PF00014; Kunitz_BPTI; 1.

DR PRINTS: PR00203; AMYLOIDA4.

DR PRINTS: PR00759; BASICPTASE.

DR SMART: SM00006; A4_EXTRA; 1.

DR SMART: SM00131; KU; 1.

DR PROSITE: PS00319; A4_EXTRA; 1.

DR PROSITE: PS00320; A4_INTRA; 1.

DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.

KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;

KW Alternative splicing; Serine protease inhibitor.

FT SIGNAL 1 17 BY SIMILARITY.

FT CHAIN 18 770

FT DOMAIN 18 699

FT TRANSMEM 700 723

FT DOMAIN 724 770

FT DOMAIN 673 715

FT SITE 287 345

FT SITE 759 762

FT DISULFID 291 341

FT DISULFID 300 324

FT DISULFID 316 337

FT CARBOHYD 542 542

FT CARBOHYD 571 571

FT VARSPLIC 289 289

FT VARSPLIC 290 364

SO SEQUENCE 770 AA; 86704 MW; C26C9D5BBD2929A7 CRC64;

Query Match Score 46; DB 1; Length 770;

Best Local Similarity 90.0%; Pred. No. 0.16;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10

DB 668 EVKMDAEFGH 677

RESULT 11

RDSL_SCHPO STANDARD: PRT: 402 AA.

ID RDSL_SCHPO

AC P53693; Q9U778;

DT 01-OCT-1996 (Rel. 34, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Rds1 protein.

GN RDS1 OR SPAC343.12.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

CC Schizosaccharomycetales; Schizosaccharomycetaceae;

OX NCBI_TaxId=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RX MEDLINE=96004765; PubMed=7565608;

RT Lucin K.M., Hilti N., Schweingruber M.E.;

RT "Schizosaccharomyces pombe rds1, an adenine-repressible gene regulated by glucose, ammonium, phosphate, carbon dioxide and temperature.";

RT Mol. Gen. Genet. 248:439-445(1995).

RL [2]

RM SEQUENCE FROM N.A.

RP STRAIN=972;

RA Murphy L., Harris D., Wood V., Rajandream M.A., Barrell B.G.;

RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases

CC -1- FUNCTION: MAY HAVE A FUNCTION IN STRESS-RELATED RESPONSES OF THE CELL.

CC -1- INDUCTION: WHEN CELLS ARE STARVED FOR GLUCOSE, AMMONIUM, OR PHOSPHATE, WHEN THEY ARE EXPOSED TO A CARBON DIOXIDE ATMOSPHERE, WHEN THEY ARE SHIFTED TO HIGHER TEMPERATURES OR WHEN THEY ENTER STATIONARY PHASE. ADENINE-REPRESSIBLE.

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CC -----

DR EMBL: X77328; CAA54544.1; -

DR EMBL: AL109739; CAB52275.1; -

DR CONFLICT 17 R -> G (IN REF. 1).

FT SEQUENCE 402 AA; 43827 MW; 564343EDD7B4BECA CRC64;

```

Query Match          66.0%; Score 35; DB 1; Length 402;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy      1 EVKMDAEFRH 10
Db      110 EAGIDAEYRH 119

RESULT 12
BICD_DROME          STANDARD;      PRT;      782 AA.
AC  P16568; O9YJDS;
DT  01-AUG-1990 (Rel. 15, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Cytoskeleton-like bicaudal D protein.
GN  BICD OR CG6605.
OS  Drosophila melanogaster (Fruit fly).
OC  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC  Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC  Ephydroidea; Drosophilidae; Drosophila.
OX  NCBI_TaxId=7227;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=90075232; PubMed=2590944;
RA  Wharton R.P., Struhl G.;
RT  "Structure of the Drosophila Bicadald protein and its role in
RT  localizing the the posterior determinant nanos.";
RL  Cell 59:881-892(1989).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=OREGON-R;
RX  MEDLINE=90152340; PubMed=2576013;
RA  Suter B., Romberg L.M., Steward R.;
RT  "Bicaudal-D, a Drosophila gene involved in developmental asymmetry:
RT  localized transcript accumulation in ovaries and sequence similarity
RT  to myosin heavy chain tail domains.";
RL  Genes Dev. 3:1957-1968(1989).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BERKELEY;
RX  MEDLINE=20196006; PubMed=10731132;
RA  Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA  Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA  George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA  Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA  Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA  Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA  Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA  Ballew R.M., Basu A.V., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA  Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA  Borkov D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA  Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA  Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA  de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA  Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA  Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
RA  Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA  Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA  Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA  Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA  Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA  Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA  Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA  Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA  Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA  Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA  Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,
RA  Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA  Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA  Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

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RA  Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA  Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA  Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA  Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA  Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA  Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA  Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT  "The genome sequence of Drosophila melanogaster.";
RL  Science 287:2185-2195(2000).
CC  -1- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR DIFFERENTIATION. IT
CC  MAY PLAY A ROLE IN LOCALIZING OF NANOS (A MATERNAL DETERMINANT)
CC  ACTIVITY IN OOCYTES. BICD MUTATIONS CAUSE NANOS MISLOCALIZATION
CC  AND THUS BICAUDAL DEVELOPMENT.
CC  -1- DEVELOPMENTAL STAGE: OOGENESIS.
CC  -1- SIMILARITY: OF C-TERMINAL HALF TO VARIOUS MYOSIN HEAVY CHAINS AND
CC  SOME INTERMEDIATE FILAMENT PROTEINS.
CC  -----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; M31684; AAA28393.1; -;
DR  EMBL; X51652; CAA35964.1; -;
DR  EMBL; AE003655; AAF53616.1; -;
DR  PIR; A33636; A33636.
DR  FLYBase; FBgn0000183; BICD.
KW  coiled coil; developmental protein.
FT  DOMAIN 3 263
FT  DOMAIN 319 477
FT  DOMAIN 601 746
FT  CONFLICT 296 296
FT  CONFLICT 318 318
FT  CONFLICT 477 477
SQ  SEQUENCE 782 AA; 88953 MW; 5A717617DF58E6 CRC64;

Query Match          66.0%; Score 35; DB 1; Length 782;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy      1 EVKMDAEFRH 10
Db      739 EMEKDEMRH 748

RESULT 13
T2S1_STRFI          STANDARD;      PRT;      269 AA.
AC  O52512;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Type II restriction enzyme SfiI (EC 3.1.21.4) (Endonuclease SfiI)
GN  R.SfiI.
OS  Streptomyces filmbiatus.
OC  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC  Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX  NCBI_TaxId=68197;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  van Cott E.M., Moran L.S., Slacko B.E., Wilson G.G.;
RT  "Characterization of the SfiI restriction and modification genes.";
RT  Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC  -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE GGCNNNNNGGCC
CC  AND CLEAVES BEFORE N-9.
CC  -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC  specific double-stranded fragments with terminal 5'-phosphates.
CC  -----
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 CC -----
 DR EMBL: AF039750; AAB95365.1; -
 DR REBASE: 1655; SflI.
 DR Hydrolyase; Endonuclease; Nuclease; Restriction system.
 SQ SEQUENCE 269 AA; 31044 MW; 3C48499BA5205EA CRC64;
 QY Query Match 64.2%; Score 34; DB 1; Length 269;
 Best Local Similarity 60.0%; Pred. No. 13;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EVKMDAEFRH 10
 Db 116 QLPMDAEFRN 125
 RESULT 14
 EFTU_BUCAL STANDARD; PRT; 394 AA.
 ID EFTU_BUCAL
 AC 031297;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Elongation factor Tu (EF-Tu).
 OS TUF OR B0526.
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 OS symbiotic bacterium).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=118099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TOKYO 1998;
 RX MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 RT Buchnera sp. APS.";
 RL Nature 407:81-86(2000).
 RN [2]
 RP SEQUENCE OF 20-384 FROM N.A.
 RX MEDLINE=98242088; PubMed=9580987;
 RA Brynne E.U., Kurland C.G., Moran N.A., Andersson S.G.;
 RT "Evolutionary rates for tuf genes in endosymbionts of aphids.";
 RL Mol. Biol. Evol. 15:574-582(1998).
 CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
 CC AMINOACYL-tRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
 CC BIOSYNTHESIS.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
 CC EF-TU/EF-1A SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: AP001119; BAB13219.1; ALT_INIT.
 DR EMBL: Y12307; CAAT2974.1; -
 DR HSSP: P02990; IETU.
 DR InterPro: IPR000795; GMP_EFTU.
 DR Pfam: PF00009; GTP_EFTU.1.
 DR PRINTS: PR00315; ELONGATINCT.
 DR PROSITE: PS00301; EFACOR_GTP.1.
 KW Elongation factor; Protein biosynthesis; GTP-binding;
 KW Complete proteome.

FT NP_BIND 19 26 GTP (BY SIMILARITY).
 FT NP_BIND 81 85 GTP (BY SIMILARITY).
 FT NP_BIND 136 139 GTP (BY SIMILARITY).
 FT CONFLICT 89 89 I -> M (IN REF. 2).
 SQ SEQUENCE 394 AA; 43465 MW; 09B73EADCA0DF5F6 CRC64;
 QY Query Match 64.2%; Score 34; DB 1; Length 394;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 VKMDAEFRH 10
 Db 68 VEYDTEFRH 76
 RESULT 15
 APB_HUMAN STANDARD; PRT; 4563 AA.
 ID APB_HUMAN
 AC P04114; 000502; Q13787;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein
 DE B-48 (Apo B-48)].
 GN APOB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87016385; PubMed=3763409;
 RA Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.;
 RA Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
 RT "Complete cDNA and derived protein sequence of human apolipoprotein
 RT B-100.";
 RL Nucleic Acids Res. 14:7501-7503(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88003974; PubMed=3652907;
 RA Ludwig E.H., Blackhart B.D., Plerotti V.R., Caiati L., Portier C.,
 RA Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
 RT "DNA sequence of the human apolipoprotein B gene.";
 RL DNA 6:363-372(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87008488; PubMed=3759943;
 RA Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
 RA Gotto A.M., Jr., Chan L.;
 RT "The complete cDNA and amino acid sequence of human apolipoprotein
 RT B-100.";
 RL J. Biol. Chem. 261:12918-12921(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87041416; PubMed=3464946;
 RA Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,
 RA Lee N., Brewer H.B., Jr.;
 RT "Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
 RT derived amino acid sequence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87161758; PubMed=3030729;
 RA Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.,
 RA Zannis V.I.;
 RT "The complete sequence and structural analysis of human
 RT apolipoprotein B-100: relationship between apob-100 and apob-48
 RT forms.";
 RL EMBO J. 5:3495-3507(1986).
 RN [6]
 RP SEQUENCE OF 709-906 FROM N.A.
 RX MEDLINE=85270450; PubMed=3860836;
 RA Deeb S.S., Motulsky A.G., Albers J.J.;

RT "A partial cDNA clone for human apolipoprotein B.":
RL Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985).
RN [17]
RP SEQUENCE OF 3056-3159 FROM N.A.
RX MEDLINE=86041888; PubMed=3903660;
RA Menabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
RT Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.;
RT "Human apolipoprotein B: identification of cDNA clones and
RT characterization of mRNA.";
RL Nucleic Acids Res. 13:6937-6953(1985).
RN [18]
RP SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A.
RX MEDLINE=86093680; PubMed=3841204;
RA Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O.,
RT Bjursell G.;
RT "Molecular cloning of human apolipoprotein B cDNA.";
RL Nucleic Acids Res. 13:8813-8826(1985).
RN [19]
RP SEQUENCE OF 3109-4563 FROM N.A.
RX MEDLINE=85300528; PubMed=2994225;
RA Knott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.F.,
RA Uredea M.S., Levy-Wilson B., Powell L.M., Pease R.J., Eddy R.,
RA Nakai H., Byers M., Priestley L.M., Robertson E., Rall L.B.,
RA Bersholtz C., Shows T.B., Mahley R.W., Scott J.;
RT "Human apolipoprotein B: structure of carboxyl-terminal domains,
RT sites of gene expression, and chromosomal localization.";
RL Science 230:37-43(1985).
RN [10]
RP SEQUENCE OF 1-291 FROM N.A.
RX MEDLINE=86143325; PubMed=3513177;
RA Procter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
RT Chen G.C., Kirshner S.W., McEnroe G., Kane J.P.;
RT "Isolation of a cDNA clone encoding the amino-terminal region of
RT human apolipoprotein B.":
RL Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986).
RN [11]
RP SEQUENCE OF 1-1670 FROM N.A.
RX MEDLINE=86287319; PubMed=346154;
RA Procter A.A., Hardman D.A., Sato K.Y., Schilling J.W.,
RA Yamanaka M., Hort Y.J., Herrild K.A., Chen G.C., Kane J.P.;
RT "Analysis of cDNA clones encoding the entire B-26 region of human
RT apolipoprotein B.":
RL Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986).
RN [12]
RP PARTIAL SEQUENCE AND IDENTIFICATION (APO-B48).
RX MEDLINE=88018019; PubMed=3659919;
RA Chen S.-H., Hahb G., Yang C.-H., Gu Z.-W., Lee B.R., Wang S.-H.,
RA Silberman S.R., Cai S.-J., Deslypere J.P., Rosseneu M.,
RA Gotto A.M. Jr., Li W.-H., Chan L.;
RT "Apolipoprotein B-48 is the product of a messenger RNA with an organ-
RT specific in-frame stop codon.";
RL Science 238:363-366(1987).
RN [13]
RP DOMAINS.
RX MEDLINE=87039351; PubMed=3773997;
RA Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,
RA Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
RA Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,
RA Levy-Wilson B., Scott J.;
RT "Complete protein sequence and identification of structural domains
RT of human apolipoprotein B.":
RL Nature 323:734-738(1986).
RN [14]
RP DOMAINS.
RX Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T.,
RA Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M.,
RA Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L.;
RT "Sequence, structure, receptor-binding domains and internal repeats
RT of human apolipoprotein B-100.";
RL Nature 323:738-742(1986).
RN [15]
RP CALCIUM-BINDING DATA.
RX MEDLINE=86242245; PubMed=3087360;

RA Dashti N., Lee D.M., Mok T.;
RT "Apolipoprotein B is a calcium binding protein.";
RL Biochem. Biophys. Res. Commun. 137:493-499(1986).
RN [16]
RP VARIANTS SER-4338.
RX MEDLINE=91071750; PubMed=1979313;
RA Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P.,
RT Cuny G., Cambien F., Roizes G.;
RT "Detection by denaturing gradient gel electrophoresis of a new
RT polymorphism in the apolipoprotein B gene.";
RL Hum. Genet. 86:91-93(1990).
RN [17]
RP VARIANTS FDB GLN-3527.
RX MEDLINE=89098975; PubMed=2563166;
RA Scoria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
RA McCarthy B.J.;
RT "Association between a specific apolipoprotein B mutation and
RT familial defective apolipoprotein B-100.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
RN [18]
RP VARIANTS LEU-2739.
RX MEDLINE=91016974; PubMed=2216805;
RA Huang L.-S., Gavish D., Breslow J.L.;
RT "Sequence polymorphism in the human apob gene at position 8344.";
RL Nucleic Acids Res. 18:5922-5922(1990).
RN [19]
RP VARIANTS FDB CYS-3558.
RX MEDLINE=95190020; PubMed=7883971;
RA Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A.,
RA Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.;
RT "Familial ligand-defective apolipoprotein B. Identification of a new
RT mutation that decreases LDL receptor binding affinity.";
RL J. Clin. Invest. 95:1225-1234(1995).
RN [20]
RP VARIANTS L-1437; S-1914; K-2566; T-3121; A-3945; M-4128 AND T-4481.
RX MEDLINE=97044521; PubMed=8889592;
RA Poirier O., Ricard S., Behague I., Souriau C., Evans A.E.,
RA Avelier D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
RT "Detection of new variants in the apolipoprotein B (Apo B) gene by
RT PCR-SSCP.";
RL Hum. Mutat. 8:282-285(1996).
RN [21]
RP VARIANTS FDB GLN-3527 AND CYS-3558.
RX MEDLINE=97403938; PubMed=9259199;
RA Rabes J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G.,
RA Kempf M., Giraudet P., Junien C., Bolleau C.;
RT "Familial ligand-defective apolipoprotein B-100: simultaneous
RT detection of the ARG3500-->GLN and ARG3531-->CYS mutations in a
RT French population.";
RL Hum. Mutat. 10:160-163(1997).
RN [22]
RP VARIANTS S-1914; R-1923; L-2739; D-3319; T-3427; Q-3432 AND I-3921.
RX MEDLINE=98141125; PubMed=9490296;
RA Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;
RT "Screening for mutations of the apolipoprotein B gene causing
RT hypocholesterolemia.";
RL Hum. Genet. 102:44-49(1998).
RN [23]
RP FUNCTION: APOLOPOPROTEIN B IS A MAJOR PROTEIN CONSTITUENT OF
CC CHYLOMICRONS, VLDL AND LDL. IT FUNCTIONS AS A RECOGNITION SIGNAL
CC FOR THE CELLULAR BINDING AND INTERNALIZATION OF LDL PARTICLES BY
CC THE APOB/E RECEPTOR.
CC -1- DISEASE: DEFECTS IN APOB ARE A CAUSE OF FAMILIAL LIGAND-DEFECTIVE
CC APOLOPOPROTEIN B-100 (FDB). IT IS A DOMINANTLY INHERITED DISORDER
CC OF LIPOPROTEIN METABOLISM LEADING TO HYPERCHOLESTEROLEMIA AND
CC INCREASED PRONESS TO CORONARY ARTERY DISEASE (CAD).
CC THE PLASMA CHOLESTEROL LEVELS ARE DRAMATICALLY ELLEVATED DUE TO
CC IMPAIRED CLEARANCE OF LDL PARTICLES BY DEFECTIVE APOB/E RECEPTORS.
CC -1- DISEASE: DEFECTS IN APOB ASSOCIATED WITH OTHER GENE DEFECTS
CC (POLYGENIC) CAN BE THE CAUSE OF HYPOCHOLESTEROLEMIA.
CC -1- MISCELLANEOUS: APO B-48 WHICH IS SYNTHESIZED ONLY BY THE
CC INTESTINE, AND FOUND IN CHYLOMICRONS, IS A SHORTENED FROM OF APO

Query Match

64.2%; Score 34; DB 1; Length 4563;

Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 EVKMDAEFR 9
| | | | : | |
Db 1483 EVKIDGQFR 1491

Search completed: October 29, 2002, 10:27:30
Job time : 7 secs

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•
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:11 : Search time 18 Seconds
(without alignments)
96.108 Million cell updates/sec

Title: US-09-580-018-5
Perfect score: 53
Sequence: 1 EVKMAEEFRH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protent:*
12: sp_virus:*
13: sp_unclassified:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	82	4	P78438
2	53	100.0	82	4	P16014
3	53	100.0	82	4	O16019
4	53	100.0	82	4	O16020
5	53	100.0	534	13	O93296
6	53	100.0	569	13	O9PV1
7	53	100.0	695	6	O95KN7
8	53	100.0	695	11	O60496
9	53	100.0	695	13	O9DGJ8
10	53	100.0	751	13	O9DGJ7
11	53	100.0	770	6	O9TU0
12	47	88.7	693	13	O98SG0
13	47	88.7	695	13	O98SF9
14	47	88.7	747	13	O91963
15	46	86.8	79	11	O35463
16	46	86.8	423	2	O52379

17	46	86.8	423	2	O45693
18	46	86.8	697	11	O99K32
19	46	86.8	695	11	P97487
20	39	73.6	142	5	O16896
21	38	71.7	427	16	O91673
22	35	66.0	582	17	O962T2
23	35	66.0	774	16	O92CV7
24	35	66.0	774	16	O92CV7
25	34	64.2	19	4	O9UCC8
26	34	64.2	28	4	O9UCD1
27	34	64.2	30	4	O9UCA9
28	34	64.2	33	4	O9UC33
29	34	64.2	105	10	O9LLJ9
30	34	64.2	239	10	O9FNG2
31	34	64.2	265	34	O9AOL8
32	34	64.2	347	12	O9LFD6
33	34	64.2	400	2	O52295
34	34	64.2	407	2	O9F8V1
35	34	64.2	431	2	O935K0
36	34	64.2	439	2	O9L5I6
37	34	64.2	454	5	O9UN07
38	34	64.2	452	5	O9Y198
39	34	64.2	475	5	O90343
40	34	64.2	612	13	O919E7
41	34	64.2	634	5	O909Y8
42	34	64.2	647	5	O62395
43	34	64.2	676	5	O9W106
44	34	64.2	738	13	O90W28
45	34	64.2	763	3	O12653

ALIGNMENTS

RESULT 1
P78438 PRELIMINARY; PRT; 82 AA.
AC P78438;
DT 01-MAY-1997 (TRENBLER, 03, Created)
DT 01-MAY-1997 (TRENBLER, 03, Last sequence update)
DT 01-MAR-2001 (TRENBLER, 16, Last annotation update)
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H., Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [2]
RP SEQUENCE OF 19-48 FROM N.A.
RA MEDLINE=87120329; PubMed=2949367;
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P., Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the Alzheimer locus.";
RL Science 235:880-884(1987).
RN [3]
RP SEQUENCE OF 32-63 FROM N.A.
RA MEDLINE=93035397; PubMed=1415269;
RA Kamino K., Orr H.T., Payami H., Witsman E.M., Alonso M.E., Pulst S.M., Anderson L., O'dahl S., Nemens E., White J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease kindreds for the APP gene region.";
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL; M29270; AAA51768.1; -.
EMBL; M29269; AAA51768.1; JOINED.

DR EMBL: M15532; AAA51564.1; -
DR EMBL: S45136; AAB23646.1; -
DR HSSP: P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match 100.0%; Score 53; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10
DB 13 EVKMDAEFRH 22

RESULT 2
O16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLROID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S60721; AAB26263.2; -
DR HSSP: P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 53; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10
DB 14 EVKMDAEFRH 23

RESULT 3
O16019 PRELIMINARY; PRT; 82 AA.
AC Q16019;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLROID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S61380; AAB26264.2; -
DR HSSP: P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 100.0%; Score 53; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10
DB 14 EVKMDAEFRH 23

RESULT 4
O16020 PRELIMINARY; PRT; 82 AA.
AC Q16020;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLROID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S61383; AAB26265.2; -
DR HSSP: P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 100.0%; Score 53; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10
DB 14 EVKMDAEFRH 23

RESULT 5
O93296 PRELIMINARY; PRT; 534 AA.
AC O93296;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLROID PROTEIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
substrate for caspase-3 in dying motoneurons";
RJ J. Neurosci. 18:5869-5880(1998).
DR EMBL: AF042098; AAC25052.1; -
DR HSSP: P05067; 1BA4.
DR Interpro: IPR001868; A4_APP.
DR PRINTS: PR00203; AMYLOID4.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.

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FT NON_TER 1 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E6D4C92 CRC64;

Query Match
Best Local Similarity 100.0%; Score 53; DB 13; Length 534;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
    |||||||
Db 432 EVKMDAEFRH 441

RESULT 6
Q9PVL1 PRELIMINARY; PRT; 569 AA.
ID Q9PVL1
AC Q9PVL1
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Coulson E.J., Paliaga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RL tells us about its function.";
RL Neurochem. Int. 0:0-0(2000).
DR EMBL: AF030341; AAF12698.1;
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOID4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match
Best Local Similarity 100.0%; Score 53; DB 13; Length 569;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
    |||||||
Db 468 EVKMDAEFRH 477

RESULT 7
Q95KN7 PRELIMINARY; PRT; 695 AA.
ID Q95KN7
AC Q95KN7
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AMYLOID B-PROTEIN PRECURSOR.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RX MEDLINE=91273117; PubMed=1905108;
RA Podlisy M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's

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RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).
DR EMBL: M58727; AAA36829.1; -.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 597 636 POTENTIAL.
SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match
Best Local Similarity 100.0%; Score 53; DB 6; Length 695;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
    |||||||
Db 593 EVKMDAEFRH 602

RESULT 8
Q60496 PRELIMINARY; PRT; 695 AA.
ID Q60496
AC Q60496
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE AMYLOID PRECURSOR PROTEIN.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing.";
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL: X97631; CAA66230.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOID4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match
Best Local Similarity 100.0%; Score 53; DB 11; Length 695;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
    |||||||
Db 593 EVKMDAEFRH 602

RESULT 9
Q9DGB8 PRELIMINARY; PRT; 695 AA.
ID Q9DGB8
AC Q9DGB8
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolosse A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms.";

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RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289218; AAG00593.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match
Best Local Similarity 100.0%; Score 53; DB 13; Length 695;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
   |||||
Db 593 EVKMDAEFRH 602

RESULT 10
ID 09DGI7 PRELIMINARY; PRT; 751 AA.
AC 09DGI7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolose A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289219; AAG00594.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match
Best Local Similarity 100.0%; Score 53; DB 13; Length 751;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
   |||||
Db 649 EVKMDAEFRH 658

RESULT 11
ID 09TUI0 PRELIMINARY; PRT; 770 AA.
AC 09TUI0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

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OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid Precursor Protein 770."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB032550; BAA84580.1; -.
DR HSSP: P05067; 1AAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BCC583E CRC64;

Query Match
Best Local Similarity 100.0%; Score 53; DB 6; Length 770;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
   |||||
Db 668 EVKMDAEFRH 677

RESULT 12
ID 098SG0 PRELIMINARY; PRT; 693 AA.
AC 098SG0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN A.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL: AJ298150; CAC37193.1; -.
DR HSSP: P05067; 1H23.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
KW Signal.
FT SIGNAL 18
SQ SEQUENCE 693 AA; 78568 MW; CAF1DF655C1AB653 CRC64;

Query Match
Best Local Similarity 88.7%; Score 47; DB 13; Length 693;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
   |||||
Db 591 EVKMDSEFRH 600

RESULT 13

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Q98SF9          PRELIMINARY;      PRT;      695 AA.
ID Q98SF9;
AC Q98SF9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN B.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL: AJ298151; CAC37194.1; -.
DR HSSP: P05067.1H23.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 695 AA; 78603 MW; DC14EB02AFB0204A CRC64;

Query Match
Best Local Similarity 88.7%; Score 47; DB 13; Length 695;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
   |||||:|:|
Db 593 EVKMDSEYRH 602

RESULT 14
Q91963          PRELIMINARY;      PRT;      747 AA.
ID Q91963;
AC Q91963;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE APP747.
GN APP747.
OS Xenopus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae.
OX NCBI_TaxID=8353;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93129227; PubMed=1282805;
RA Okada H., Okamoto H.;
RT "A Xenopus homologue of the human beta-amyloid precursor protein:
RT developmental regulation of its gene expression.";
RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
DR EMBL: S52417; AAB24853.1; -.
DR HSSP: P05067.1H23.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.

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DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 747 AA; 84893 MW; A75E81885681D948 CRC64;

Query Match
Best Local Similarity 88.7%; Score 47; DB 13; Length 747;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
   |||||:|:|
Db 645 EVKMDSEYRH 654

RESULT 15
Q03463          PRELIMINARY;      PRT;      79 AA.
ID Q03463;
AC Q03463;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).
GN BETA APP.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Sambamurti K., Plinix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF030413; AAB86608.1; -.
DR HSSP: P05067.1BA4.
FT NON_TER
FT NON_TER
SQ SEQUENCE 79 AA; 8538 MW; 37F2CC63BFF3F597 CRC64;

Query Match
Best Local Similarity 86.8%; Score 46; DB 11; Length 79;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
   |||||:|:|
Db 17 EVKMDSEYRH 26

Search completed: October 29, 2002, 10:29:42
Job time : 19.1429 secs

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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:56 : Search time 9 Seconds
(Without alignments)
27.140 Million cell updates/sec

Title: US-09-580-018-5
Perfect score: 53
Sequence: 1 EVKMDAEFRH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backt1test1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	12	5	PCT-US94-07043A-2
2	53	100.0	16	5	PCT-US94-07043A-1
3	53	100.0	27	1	US-08-141-374-11
4	53	100.0	27	1	US-08-541-902-11
5	53	100.0	45	1	US-08-462-859A-5
6	53	100.0	45	1	US-08-123-659A-5
7	53	100.0	45	1	US-08-464-247A-5
8	53	100.0	45	1	US-08-464-248A-5
9	53	100.0	58	1	US-08-371-930-25
10	53	100.0	58	5	PCT-US94-01712-25
11	53	100.0	59	1	US-08-484-969-3
12	53	100.0	59	1	US-08-472-627-3
13	53	100.0	59	1	US-08-388-463-3
14	53	100.0	63	1	US-08-462-859A-3
15	53	100.0	63	1	US-08-462-859A-4
16	53	100.0	63	1	US-08-123-659A-4
17	53	100.0	63	1	US-08-123-659A-4
18	53	100.0	63	1	US-08-464-247A-3
19	53	100.0	63	1	US-08-464-247A-4
20	53	100.0	63	1	US-08-464-248A-3
21	53	100.0	63	1	US-08-464-248A-4
22	53	100.0	103	2	US-08-404-831-2
23	53	100.0	103	2	US-08-612-785B-2
24	53	100.0	103	2	US-08-475-579A-2
25	53	100.0	103	2	US-08-920-162A-2
26	53	100.0	103	3	US-08-339-708A-10
27	53	100.0	103	4	US-09-356-931-2

28	53	100.0	103	4	US-08-703-675C-2	Sequence 2, Appl1
29	53	100.0	103	4	US-08-617-267C-2	Sequence 2, Appl1
30	53	100.0	105	2	US-08-729-345-1	Sequence 1, Appl1
31	53	100.0	117	2	US-08-729-345-3	Sequence 3, Appl1
32	53	100.0	152	6	5187153-4	Patent No. 5187153
33	53	100.0	162	6	5220013-4	Patent No. 5220013
34	53	100.0	162	6	5223482-4	Patent No. 5223482
35	53	100.0	264	1	US-07-990-893-5	Sequence 5, Appl1
36	53	100.0	487	1	US-08-462-859A-9	Sequence 9, Appl1
37	53	100.0	487	1	US-08-123-659A-9	Sequence 9, Appl1
38	53	100.0	487	1	US-08-464-247A-9	Sequence 9, Appl1
39	53	100.0	487	1	US-08-464-248A-9	Sequence 9, Appl1
40	53	100.0	492	1	US-08-462-859A-7	Sequence 7, Appl1
41	53	100.0	492	1	US-08-123-659A-7	Sequence 7, Appl1
42	53	100.0	492	1	US-08-464-247A-7	Sequence 7, Appl1
43	53	100.0	492	1	US-08-464-248A-7	Sequence 7, Appl1
44	53	100.0	537	1	US-08-453-552-4	Sequence 4, Appl1
45	53	100.0	537	2	US-08-710-637-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
PCT-US94-07043A-2
Sequence 2, Application PC/TUS9407043A
GENERAL INFORMATION:
APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,
APPLICANT: Dieter; Dreyer, Robert N.; Koehnig, Gerhard
TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC
TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miles Inc.
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
COMPUTER: Sharp PC 4600
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07043A
FILING DATE: June 21, 1994
CLASSIFICATION:
APPLICATION NUMBER: PCT/US93/10889
FILING DATE: November 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/995,660
FILING DATE: December 16, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/880,914
FILING DATE: May 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Pamela A. Simonon
REGISTRATION NUMBER: 31,060
REFERENCE/DOCKET NUMBER: MTI 224.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 937-2340
TELEFAX: (203) 937-2795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-07043A-2
Query Match 100.0%; Score 53; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00016;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
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 Db 3 EVKMDAEFRH 12

RESULT 2

PCT-US94-07043A-1
 ; Sequence 1, Application PC/TUS9407043A

;; GENERAL INFORMATION:
 ; APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,
 ; APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard
 ; TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC
 ; TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Miles Inc.
 ; STREET: 400 Morgan Lane
 ; CITY: West Haven
 ; STATE: Connecticut
 ; COUNTRY: USA
 ; ZIP: 06516
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
 ; COMPUTER: Sharp PC 4600
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: Wordperfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/07043A
 ; FILING DATE: June 21, 1994
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/10889
 ; FILING DATE: November 12, 1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/995,660
 ; FILING DATE: December 16, 1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/880,914
 ; FILING DATE: May 11, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pamela A. Simonton
 ; REGISTRATION NUMBER: 31,060
 ; REFERENCE/DOCKET NUMBER: MTI 224.3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (203) 937-2340
 ; TELEFAX: (203) 937-2795
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; PCT-US94-07043A-1

Query Match 100.0%; Score 53; DB 5; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.00021;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
 |||||
 Db 3 EVKMDAEFRH 12

RESULT 3

US-08-141-324-11
 ; Sequence 11, Application US/08141324

;; GENERAL INFORMATION:
 ; APPLICANT: Travls, James
 ; APPLICANT: Potempa, Jan S.
 ; APPLICANT: Barr, Philip J.
 ; APPLICANT: Pavloff, Nadine

;; APPLICANT: Pike, Robert N.
 ; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
 ; TITLE OF INVENTION: Protease
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Greenlee and Winner, P.C.
 ; STREET: 5370 Manhattan Circle, Suite 201
 ; CITY: Boulder
 ; STATE: CO
 ; COUNTRY: US

;; ZIP: 80303
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/141,324
 ; FILING DATE: 21-OCT-1993
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ferber, Donna M.
 ; REGISTRATION NUMBER: 33,878
 ; REFERENCE/DOCKET NUMBER: 44-93
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 303-499-8080
 ; TELEFAX: 303-499-8089
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 27 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; US-08-141-324-11

Query Match 100.0%; Score 53; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
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 Db 5 EVKMDAEFRH 14

RESULT 4

US-08-541-902-11
 ; Sequence 11, Application US/08541902

;; GENERAL INFORMATION:
 ; APPLICANT: Travls, James
 ; APPLICANT: Potempa, Jan S.
 ; APPLICANT: Barr, Philip J.
 ; APPLICANT: Pavloff, Nadine
 ; APPLICANT: Pike, Robert N.
 ; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
 ; TITLE OF INVENTION: Protease
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Greenlee and Winner, P.C.
 ; STREET: 5370 Manhattan Circle, Suite 201
 ; CITY: Boulder
 ; STATE: CO
 ; COUNTRY: US
 ; ZIP: 80303
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/541,902
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/141,324
FILING DATE: 21-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Felder, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 44-93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
ANT-SENSE: NO
US-08-541-902-11

Query Match 100.0%; Score 53; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
Db 5 EVKMDAEFRH 14

RESULT 5
US-08-462-859A-5
Sequence 5, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-462-859A-5

Query Match 100.0%; Score 53; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
Db 6 EVKMDAEFRH 15

RESULT 6
US-08-123-659A-5
Sequence 5, Application US/08123659A
Patent No. 5656477
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-5

Query Match 100.0%; Score 53; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEFRH 10
Db 6 EVKMDAEFRH 15

RESULT 7
US-08-464-247A-5
Sequence 5, Application US/08464247A
Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
of B-Amyloid Peptide

```
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-5

Query Match      100.0%; Score 53; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVKMDAEFRH 10
        |||
Db      6 EVKMDAEFRH 15

RESULT 8
US-08-464-248A-5
Sequence 5, Application US/08464248A
Patent No. 5703209
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Agents to Access Agents Which Down-Regulate Formation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-5

Query Match      100.0%; Score 53; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVKMDAEFRH 10
        |||
Db      6 EVKMDAEFRH 15

RESULT 9
US-08-371-930-25
Sequence 25, Application US/08371930
Patent No. 5578451
GENERAL INFORMATION:
APPLICANT: Nishimoto, Ikuro
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,930
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/019,208
FILING DATE: February 18, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/154001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 58
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-371-930-25

Query Match      100.0%; Score 53; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVKMDAEFRH 10
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Db      43 EVKMDAEFRH 52
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RESULT 10
PCT-US94-01712-25
Sequence 25, Application PC/TUS9401712
GENERAL INFORMATION:
APPLICANT: Nishimoto, Ikuro
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/019,208
FILING DATE: February 18, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/154001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO.: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 58
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US94-01712-25
Query Match 100.0%; Score 53; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVKMDAEFRH 10
DB 43 EVKMDAEFRH 52

RESULT 11
US-08-484-969-3
Sequence 3, Application US/08484969
Patent No. 5679531
GENERAL INFORMATION:
APPLICANT: Konig, Gerhard
TITLE OF INVENTION: Monoclonal Antibody Specific for BA4
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,969
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 95,216
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ. ID NO.: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 4..5
OTHER INFORMATION: /label= Beta
OTHER INFORMATION: /note= "Beta cleavage site in App"
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 20..21
OTHER INFORMATION: /label= Alpha
OTHER INFORMATION: /note= "Alpha cleavage site in App, residues 16/17
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 46..47
OTHER INFORMATION: /label= Gamma
OTHER INFORMATION: /note= "Gamma cleavage site in App"
FEATURE:
NAME/KEY: Peptide
LOCATION: 5..47
OTHER INFORMATION: /label= BA4
OTHER INFORMATION: /note= "BA4 peptide"
FEATURE:
NAME/KEY: Region
LOCATION: 33..56
OTHER INFORMATION: /label= Tm
OTHER INFORMATION: /note= "Transmembrane region of App"
FEATURE:
NAME/KEY: Region
LOCATION: 1..32
OTHER INFORMATION: /label= Ex
OTHER INFORMATION: /note= "N-terminal extracellular part of App"
US-08-484-969-3
Query Match 100.0%; Score 53; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVKMDAEFRH 10
DB 1 EVKMDAEFRH 10

RESULT 12
US-08-472-627-3
Sequence 3, Application US/08472627
Patent No. 5693753
GENERAL INFORMATION:
APPLICANT: Konig, Gerhard
TITLE OF INVENTION: Monoclonal Antibody Specific for BA4
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive Suite 3000

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,627
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McDowell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 95,216
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1234
TELEFAX: 312-715-1000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 4..5
OTHER INFORMATION: /label= Beta
OTHER INFORMATION: /note= "Beta cleavage site in App"
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 20..21
OTHER INFORMATION: /label= Alpha
OTHER INFORMATION: /note= "Alpha cleavage site in App, residues 16/17"
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 46..47
OTHER INFORMATION: /label= Gamma
OTHER INFORMATION: /note= "Gamma cleavage site in App"
FEATURE:
NAME/KEY: Peptide
LOCATION: 5..47
OTHER INFORMATION: /label= BA4
OTHER INFORMATION: /note= "BA4 peptide"
FEATURE:
NAME/KEY: Region
LOCATION: 33..56
OTHER INFORMATION: /label= Tm
OTHER INFORMATION: /note= "Transmembrane region of App"
FEATURE:
NAME/KEY: Region
LOCATION: 1..32
OTHER INFORMATION: /label= Ex
OTHER INFORMATION: /note= "N-terminal extracellular part of App"
US-08-472-627-3
Query Match 100.0%; Score 53; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVKMDAEFRH 10
Db 1 EVKMDAEFRH 10

RESULT 13
US-08-388-463-3
Sequence 3, Application US/08388463
Patent No. 5786180

GENERAL INFORMATION:
APPLICANT: Konig, Gerhard
TITLE OF INVENTION: Monoclonal Antibody Specific for BA4
TITLE OF INVENTION: Peptide
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: Illinois
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,463
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDowell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 95,216
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 4..5
OTHER INFORMATION: /label= Beta
OTHER INFORMATION: /note= "Beta cleavage site in App"
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 20..21
OTHER INFORMATION: /label= Alpha
OTHER INFORMATION: /note= "Alpha cleavage site in App, residues 16/17"
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 46..47
OTHER INFORMATION: /label= Gamma
OTHER INFORMATION: /note= "Gamma cleavage site in App"
FEATURE:
NAME/KEY: Peptide
LOCATION: 5..47
OTHER INFORMATION: /label= BA4
OTHER INFORMATION: /note= "BA4 peptide"
FEATURE:
NAME/KEY: Region
LOCATION: 33..56
OTHER INFORMATION: /label= Tm
OTHER INFORMATION: /note= "Transmembrane region of App"
FEATURE:
NAME/KEY: Region
LOCATION: 1..32
OTHER INFORMATION: /label= Ex
OTHER INFORMATION: /note= "N-terminal extracellular part of App"
US-08-388-463-3
Query Match 100.0%; Score 53; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10
| | | | |
Db 1 EVKMDAEFRH 10

RESULT 14
US-08-462-859A-3
; Sequence 3, Application US/08462859A
; Patent No. 5652092

; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-462-859A-3

Query Match 100.0%; Score 53; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10
| | | | |
Db 6 EVKMDAEFRH 15

RESULT 15
US-08-462-859A-4
; Sequence 4, Application US/08462859A
; Patent No. 5652092

; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey

; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-462-859A-4

Query Match 100.0%; Score 53; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EVKMDAEFRH 10
| | | | |
Db 6 EVKMDAEFRH 15

Search completed: October 29, 2002, 10:32:07
Job time : 9 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: October 29, 2002, 10:22:21 ; Search time 23.1429 Seconds
(without alignments)
47.995 Million cell updates/sec

Title: US-09-580-018-6

Perfect score: 54

Sequence: 1 VKMDAEFRHD 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	10	22	AAAB46210
2	54	100.0	16	21	AAAB06315
3	54	100.0	16	21	AAAB06317
4	54	100.0	18	16	AAAR75696
5	54	100.0	18	22	AAED00608
6	54	100.0	19	12	AAAR14135
7	54	100.0	20	21	AAAG6713
8	54	100.0	33	21	AAAG68002
9	54	100.0	39	21	AAAG69717
10	54	100.0	45	18	AAW26512
11	54	100.0	45	18	AAW26392

12	54	100.0	45	19	AAW44748	APP-REP 751 [BAP d
13	54	100.0	45	19	AAW42977	Deletion beta-amy1
14	54	100.0	46	22	AAAB37523	Amyloid precursor
15	54	100.0	53	15	AAAR5695	Sequence of uniden
16	54	100.0	53	15	AAAR5696	Sequence of uniden
17	54	100.0	53	15	AAAR5697	Sequence of uniden
18	54	100.0	53	16	AAAR6468	Variant beta amylo
19	54	100.0	54	21	AAAB32126	Amyloid-beta precu
20	54	100.0	57	21	AAAB10910	Human amyloid prec
21	54	100.0	58	15	AAAR58937	Amyloid precursor
22	54	100.0	59	17	AAW05375	Beta-amyloid precu
23	54	100.0	59	19	AAW70863	Beta-amyloid precu
24	54	100.0	59	22	AAAB84425	Partial sequence o
25	54	100.0	60	21	AAAG69701	Beta-amyloid precu
26	54	100.0	63	18	AAW26511	Amyloid precursor
27	54	100.0	63	18	AAW26391	Amyloid precursor
28	54	100.0	63	19	AAW44747	APP-REP 751 BAP pe
29	54	100.0	63	19	AAW44746	APP-REP 751 [BAP E
30	54	100.0	63	19	AAW42975	Beta-amyloid pepti
31	54	100.0	63	19	AAW42976	Beta-amyloid pepti
32	54	100.0	67	19	AAW71377	Peptide derived fr
33	54	100.0	93	22	ABG19083	Novel human diagno
34	54	100.0	103	16	AAAR74697	Beta-amyloid precu
35	54	100.0	103	19	AAW51317	Natural beta-amylo
36	54	100.0	103	20	AAW89372	Beta-amyloid pepti
37	54	100.0	103	20	AAW56103	Beta-amyloid precu
38	54	100.0	103	22	AAAR12509	Beta-amyloid precu
39	54	100.0	104	19	AAW51100	Amino acid sequenc
40	54	100.0	112	17	AAAR33556	Familial Alzheimer
41	54	100.0	115	20	AAW97999	London-FAD APP pol
42	54	100.0	117	19	AAW51102	Flag-amyloid prote
43	54	100.0	162	9	AAAR8151	Deduced sequence 1
44	54	100.0	162	12	AAAR10023	Beta-amyloid relat
45	54	100.0	162	14	AAAR37863	Deduced from clone

ALIGNMENTS

RESULT 1
ID AAB46210 standard; peptide: 10 AA.
AC AAB46210;
XX
XX
04-APR-2001 (first entry)
XX
DE Human APP derived immunogenic peptide #6.
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN W0200072880-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14810.
XX
PR 28-MAY-1999; 99US-0322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DR, Bard F, Vasquez NT, Yednock T;
XX WPT: 2001-032104/04.
XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid
PT specific antibody -
XX

PS Disclosure: Figure 19; 143pp; English.

CC This invention describes a novel method of preventing or treating a

CC disease associated with amyloid deposits of amyloid precursor protein

CC (APP) Abeta fragments in the brain of a patient, which comprises

CC administering to the patient: (a) an antibody that binds to Abeta, the

CC antibody binds to an amyloid deposit and induces a clearing response (Fc

CC receptor mediated phagocytosis) against it (b) a polypeptide containing

CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent

CC that induces an immunogenic response against residues 1-3 to 7-11 of

CC Abeta. The products of the invention have neurotropic and neuroprotective

CC activity. The method is also useful for monitoring a course of treatment

CC being administered to a patient e.g. active and passive immunization. The

CC methods are useful for prophylactic and therapeutic treatment of

CC Alzheimer's disease.

XX

SQ Sequence 10 AA:

Query Match 100.0%; Score 54; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00024;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10

DB 1 VKMDAEFRHD 10

RESULT 2

AAB06315

ID AAB06315 standard; peptide; 16 AA.

XX

AC AAB06315;

XX

DT 03-OCT-2000 (first entry)

XX

DE Human beta-amyloid precursor protein beta-secretase cleavage site.

XX

OS Homo sapiens.

XX

FT Key Location/Qualifiers

FT Cleavage-site 8..9

XX

PN WO200026348-A2.

XX

PD 11-MAY-2000.

XX

PF 04-NOV-1999; 99WO-CA01058.

XX

PR 04-NOV-1998; 98CA-2249648.

XX

PA (RECL-) INST RECH CLINIQUES MONTREAL.

XX

PI Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

XX

DR WPI; 2000-365601/31.

XX

PT Novel soluble proteic fragment of subtilisin-kexin isoenzyme for

PT producing a polypeptide useful for treating hypercholesterolemia, liver

PT steatosis and amyloidosis, comprises a specific amino acid sequence -

XX

PS Example 4; Page 51; 119pp; English.

XX

CC The present sequence is the beta-secretase site of human beta-amyloid

CC precursor protein (beta-APP). The sequence may be cleaved

CC by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1

CC (SKI-1), a type-I membrane-bound proteinase. Peptides which bind to and

CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for

CC screening inhibitors of SKI-1 activity, or for screening enhancers of

CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1

CC catalytic site may be used as inhibitors of SKI-1 activity. They may be

CC used to treat diseases involving overexpression of SKI-1 or SKI-1

CC substrate. Such diseases include hypercholesterolemia, high levels of

CC fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,

CC Ras-dependent cancer, restenosis and amyloid protein formation.

XX

SQ Sequence 16 AA:

Query Match 100.0%; Score 54; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.0004;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10

DB 6 VKMDAEFRHD 15

RESULT 3

AAB06317

ID AAB06317 standard; peptide; 16 AA.

XX

AC AAB06317;

XX

DT 03-OCT-2000 (first entry)

XX

DE Human beta-amyloid precursor protein beta-epsiloni-secretase site.

XX

OS Homo sapiens.

XX

FT Key Location/Qualifiers

FT Cleavage-site 8..9

XX

PN WO200026348-A2.

XX

PD 11-MAY-2000.

XX

PF 04-NOV-1999; 99WO-CA01058.

XX

PR 04-NOV-1998; 98CA-2249648.

XX

PA (RECL-) INST RECH CLINIQUES MONTREAL.

XX

PI Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

XX

DR WPI; 2000-365601/31.

XX

PT Novel soluble proteic fragment of subtilisin-kexin isoenzyme for

PT producing a polypeptide useful for treating hypercholesterolemia, liver

PT steatosis and amyloidosis, comprises a specific amino acid sequence -

XX

PS Example 4; Page 51; 119pp; English.

XX

CC The present sequence is the beta-epsiloni-secretase site of human

CC beta-amyloid precursor protein (beta-APP). The sequence may be cleaved

CC by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1

CC (SKI-1), a type-I membrane-bound proteinase. Peptides which bind to and

CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for

CC screening inhibitors of SKI-1 activity, or for screening enhancers of

CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1

CC catalytic site may be used as inhibitors of SKI-1 activity. They may be

CC used to treat diseases involving overexpression of SKI-1 or SKI-1

CC substrate. Such diseases include hypercholesterolemia, high levels of

CC fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,

CC Ras-dependent cancer, restenosis and amyloid protein formation.
XX Sequence 16 AA;
SQ

Query Match 100.0%; Score 54; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
DB 4 VKMDAEFRHD 13

RESULT 4
AAR75696
ID AAR75696 standard; peptide; 18 AA.
XX
AC AAR75696;
XX
DT 21-JAN-1996 (first entry)
XX
DE Unspecified peptide.
XX
KM Amyloid precursor protein; APP; annexin-V; Alzheimer's disease;
KM disease diagnosis; therapy; antibody.
XX
OS Synthetic.
XX
PM EP655626-A1.
XX
PD 31-MAY-1995.
XX
PF 10-NOV-1994; 94EP-0308309.
XX
PR 10-NOV-1993; 93US-0149975.
XX
PA (MCLF-) MCLEAN HOSPITAL CORP.
XX
PI Honda T, Nixon R;
DR WPI; 1995-195688/26.
XX
PT New peptide(s) associated with Alzheimer's disease - namely p33 and
PT the amyloid precursor C2 fragment, useful for the prodn. of
PT diagnostic antibodies
XX
PS Disclosure; Page 13; 32pp; English.
XX
CC Unspecified peptide.
CC
SQ Sequence 18 AA;
XX

Query Match 100.0%; Score 54; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
DB 1 VKMDAEFRHD 10

RESULT 5
AAE00608
ID AAE00608 standard; peptide; 18 AA.
XX
AC AAE00608;
XX
DT 02-JUL-2001 (first entry)
XX
DE Beta-amyloid precursor protein beta-secretase cleavage site.
XX
KM Beta-amyloid precursor protein; beta-APP; caspase; beta-secretase;
KM cysteine protease; apoptosis; caspase expression cassette; metastasis;

KW tumour; cathepsin B; urokinase; proliferation; gene therapy;
KW interdomain linker; cleavage site; Alzheimer's disease.
XX
XX Unidentified.
XX
PN WO200129232-A2.
XX
PD 26-APR-2001.
XX
PF 19-OCT-2000; 2000WO-US28941.
XX
PR 20-OCT-1999; 99US-0160559.
PR 14-AUG-2000; 2000US-0225564.
XX
PA (SCIO-) SCIOS INC.
XX
PI Cordell B, Li Y;
XX
DR WPI; 2001-290920/30.
XX
XX
PF Novel fusion polypeptide comprising first and second caspase subunit
PF separated by cleavage site not associated in nature with caspase
PT subunit, useful for cloning gene encoding enzymes involved in
PT proteolytic cleavage
XX
XX
PS Example 2; Page 26; 116pp; English.
XX
CC The present sequence is a beta-secretase cleavage site of beta-amyloid
CC precursor protein (beta-APP). This sequence is used to construct
CC an artificially engineered chimeric cassette comprising human caspase-3
CC with interdomain linker replaced by Swedish mutant beta-secretase
CC cleavage site. This modified caspase-3 plays a pivotal role in
CC Alzheimer's disease. Caspases are a family of cysteine proteases, that
CC participate in the initiation and execution of apoptosis.
CC The present invention relates to a method for functional cloning of genes
CC encoding proteins or enzymes involved in proteolytic cleavage. The
CC invention is based on the use of caspase expression cassettes comprising
CC the coding sequence of a proteolytic cleavage site flanked by sequences
CC encoding two caspase subunits. A fusion polypeptide comprising a first
CC and a second caspase subunit, separated by a cleavage site not associated
CC in nature, is useful for cloning gene encoding enzymes involved in
CC proteolytic cleavage. An expression cassette containing fusion
CC polypeptide is used to identify a mutant cell line deficient in an
CC enzyme of interest and is also useful for diagnosis and suppression of
CC proliferation or metastases of a tumour cell characterised by
CC overexpression of a polypeptide (e.g. Cathepsin B or urokinase,
CC selectively expressed in the tumour cells). DNA encoding fusion
CC polypeptide is used in gene therapy.
XX
SQ Sequence 18 AA;
XX

Query Match 100.0%; Score 54; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
DB 8 VKMDAEFRHD 17

RESULT 6
AAR14135
ID AAR14135 standard; peptide; 19 AA.
XX
AC AAR14135;
XX
DT 12-DEC-1991 (first entry)
XX
DE Brain-derived protease substrate contg. beta-APP cleavage site.
XX
KM Alzheimer's disease; chymase; multicatalytic protease;
KM beta-amyloid precursor protein; A4.
XX

OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 4..5
 FT /note= "chymase and multicatalytic protease site"
 XX
 XX
 PN WO9113904-A.
 PD 19-SEP-1991.
 XX
 PF 04-MAR-1991; 91WO-US01474.
 PR
 XX 05-MAR-1990; 90US-0489290.
 XX
 PA (CEPH-) CEPHALON INC.
 XX
 PI Siman R, Nelson RB, Kauer J, Potter H;
 XX
 DR WPI; 1991-295576/40.
 XX
 PT New chymotrypsin-like serine protease(s) - and their inhibitors
 PT are used to treat Alzheimer's disease
 XX
 PS Claim 41: Page 63; 86pp; English.
 XX
 CC This peptide is designed based on the sequence of beta-APP A4
 CC cleavage site. Cleavage by proteases in the brain releases beta-
 CC amyloid protein, the deposition of which is a feature of Alzheimer's
 CC disease neuropathology. The peptide is used to screen for candidate
 CC proteases which cleave between the Met and Asp residues. Two new
 CC proteases have been isolated having this cleavage specificity.
 CC Chymase was isolated from rat brains and multicatalytic protease was
 CC isolated from human cerebral cortex. See also AAR14136-9.
 XX
 SQ Sequence 19 AA:
 Query Match 100.0%; Score 54; DB 12; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0.00048;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VKMDAEFRHD 10
 |||||||||
 Db 2 VKMDAEFRHD 11
 RESULT 7
 AAY69713
 ID AAY69713 standard; peptide; 20 AA.
 XX
 AC AAY69713;
 XX
 DT 11-APR-2000 (first entry)
 XX
 DE Beta-APP alpha-secretase substrate [KM]-APP(-10,+10).
 XX
 KM Noctropic; neuroprotective; beta-amyloid precursor protein; metabolism;
 KM cleavage site; beta-secretase; neurodegenerative disease;
 KM Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO9964587-A1.
 XX
 PD 16-DEC-1999.
 XX
 PF 04-JUN-1999; 99WO-FR01326.
 XX
 PR 05-JUN-1998; 98FR-0007068.
 PR 31-MAR-1999; 99US-0122599.
 XX
 PA (RHON) RHONE-POULENC RORER SA.
 PA (UYPA-) UNIV CURIE PARIS VI P & M.
 XX

PI Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
 DR WPI; 2000-097537/08.
 XX
 PT Polypeptide with beta-secretase activity, specific for wild-type
 PT amyloid precursor protein, useful in treating Alzheimer's disease -
 XX
 PS Example 3; Page 24; 44pp; French.
 XX
 CC Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
 CC novel polypeptide with beta-secretase activity that can cleave
 CC specifically the natural beta-amyloid precursor protein (BAPP). Normal
 CC cleavage of the protein occurs between amino acids Met596-Asp597 and
 CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
 CC polypeptide is used to identify agents that interact specifically with
 CC it. These agents regulate metabolism of APP, particularly they slow down
 CC or reduce production of beta-amyloid, so can be used to treat
 CC neurodegenerative diseases, particularly Alzheimer's disease.
 XX
 SQ Sequence 20 AA:
 Query Match 100.0%; Score 54; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.00051;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VKMDAEFRHD 10
 |||||||||
 Db 8 VKMDAEFRHD 17
 RESULT 8
 AAW98002
 ID AAW98002 standard; Protein; 33 AA.
 XX
 AC AAW98002;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Amyloid precursor protein (aa656-678) with Swedish mutation.
 XX
 KM Amyloid precursor protein; APP; human; gene targeting;
 KM homologous recombination; transgenic mouse; transgenic animal;
 KM animal model; Alzheimer's disease.
 XX
 OS Mus musculus.
 XX
 PN WO9909150-A1.
 XX
 PD 25-FEB-1999.
 XX
 PF 18-AUG-1997; 97WO-US14507.
 XX
 PR 18-AUG-1997; 97WO-US14507.
 XX
 PA (FARB) BAYER CORP.
 XX
 PI Wirak DO;
 XX
 DR WPI; 1999-181029/15.
 XX
 PT Modification of target nucleic acids - by homologous recombination,
 PT used particularly for introducing a humanised amyloid precursor
 PT protein gene into rodents for producing models of Alzheimer's
 PT disease
 XX
 PS Disclosure; Page 145; 209pp; English.
 XX
 CC This polypeptide comprises residues 656-678 of a murine amyloid
 CC precursor protein (APP). The invention provides a novel gene
 CC targeting strategy that facilitates the introduction of one or
 CC more specific mutations into any gene in a single double reciprocal
 CC homologous recombination step. The method has been used
 CC particularly for introducing a humanised APP gene into rodents for

CC producing animal models of Alzheimer's disease (AD). 4 independent
CC lines of transgenic mice (lines ES5007, ES5103, ES5401 and ES5403)
CC have been created using the gene targeting technique applied to
CC embryonic stem cells. In each line, the mouse APP gene was modified
CC to encode a mouse/human hybrid (m/hAPP) where amino acid residues
CC 666-770 of APP770 were encoded by human cDNA sequences instead of
CC mouse genomic exons (exons 16-18). Within these residues, only 3
CC amino acid differences exist between the mouse and human proteins,
CC i.e. Gly-676 to Arg, Phe-681 to Thr and Arg-684 to His. The
CC exon-cDNA fusion gene therefore encodes an APP containing a
CC humanised beta-amyloid domain. Swedish and/or London-PAD APP
CC mutations have also been introduced (see also AAW97997-W98001).

Sequence 33 AA;

Query Match 100.0%; Score 54; DB 20; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10
| | | | | | | | | |
Db 14 VKMDAEFRHD 23

RESULT 9

ID AAY69717 standard; peptide: 39 AA.

AC AAY69717;

DT 11-APR-2000 (first entry)

DE Beta-APP alpha-secretase substrate [KM]-APP(-20,+20).

KM Neurotrophic; neuroprotective; beta-amyloid precursor protein; metabolism;

KW cleavage site; beta-secretase; neurodegenerative disease;

OS Alzheimer's disease.

OS Homo sapiens.

XX MO9964587-A1.

XX 16-DEC-1999.

XX 04-JUN-1999; 99MO-FR01326.

XX 05-JUN-1998; 98PR-0007068.

XX 31-MAR-1999; 99US-0122599.

PA (RHON) RHONE-POULENC RORER SA.

PA (UYPA-) UNIV CURIE PARIS VI P 6 M.

PI Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;

DR WPI; 2000-097537/08.

XX Polypeptide with beta-secretase activity, specific for wild-type

PT amyloid precursor protein, useful in treating Alzheimer's disease

XX Example 3; Page 24; 44pp; French.

XX Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
CC novel polypeptide with beta-secretase activity that can cleave
CC specifically the natural beta-amyloid precursor protein (bAPP). Normal
CC cleavage of the protein occurs between amino acids Met596-Asp597 and
CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
CC polypeptide is used to identify agents that interact specifically with
CC it. These agents regulate metabolism of APP, particularly they slow down
CC or reduce production of beta-amyloid, so can be used to treat
CC neurodegenerative diseases, particularly Alzheimer's disease.

Sequence 39 AA;

Query Match 100.0%; Score 54; DB 21; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10
| | | | | | | | | |
Db 17 VKMDAEFRHD 26

RESULT 10

ID AAW26512 standard; peptide: 45 AA.

AC AAW26512;

DT 06-JAN-1998 (first entry)

DE Amyloid precursor protein fragment APP-REP 751 (BAP del11-28).

KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;

KW substrate; muten; secretase; Alzheimer's disease; human.

OS Chimeric Homo sapiens.

OS Chimeric synthetic.

FT Key Location/Qualifiers

FT Cleavage-site 7..8 /note= "secretase cleavage site"

FT Peptide 10..33 /label= BAP(del11-28)

FT Domain 20..42 /note= "truncated beta-amyloid protein"

FT /label= Transmembrane

PN US5656477-A.

XX 12-AUG-1997.

XX 01-MAY-1992; 92US-0877675.

XX 20-SEP-1993; 93US-0123659.

XX 01-MAY-1992; 92US-0877675.

PA (AMCY) AMERICAN CYANAMID CO.

PI Jacobsen JS, Vitek MP;

DR WPI; 1997-414594/38.

XX Nucleic acid encoding amyloid precursor muten(s) - comprising

PT reporter gene and coding sequence, for identifying compounds which

PT modify the activity of proteolytic enzymes which cleave APP

XX Disclosure; Fig 5A; 84pp; English.

XX This peptide sequence shows the region of amyloid precursor protein
CC (APP) that includes a truncated beta-amyloid protein (BAP) lacking
CC the native secretase cleavage/recognition site. In an attempt to
CC engineer an APP non-cleavable substrate for secretase, an
CC APP-reporter (APP-REP) protein that carries the BAP deletion has
CC been expressed in recombinant host cells. Deletion of these 18
CC amino acids, however, still resulted in the secretion of an
CC N-terminal APP-reporter fragment into the cytoplasm. Non-
CC cleavable APP substrates can be used to detect other putative
CC abnormal APP processing events. They can also be used to
CC investigate cellular post-translational modifications to APP in
CC order to determine the potential influence on normal secretase and
CC abnormal BAP 'clipping' activities.

Sequence 45 AA;

Query Match 100.0%; Score 54; DB 18; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0012;


```
RESULT 13
AAM42977
ID AAM42977 standard; peptide; 45 AA.
XX
XX AAM42977;
AC
XX 01-MAY-1998 (first entry)
XX
XX Deletion beta-amyloid peptide (BAP) derived from APP-REP 751.
DE
XX
XX Beta-amyloid peptide; BAP; extracellular BAP plaque;
KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;
KW amyloid precursor protein; APP; secretase; BAP aggregation;
KW abnormal proteolytic cleavage.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX FT Domain 20..43
XX FT /note= "putative transmembrane domain"
XX
XX US5703209-A.
XX
XX 30-DEC-1997.
XX
XX 05-JUN-1995; 95US-0464248.
XX
XX 20-SEP-1993; 93US-0123659.
XX PR 01-MAY-1992; 92US-0877675.
XX
XX (AMCY ) AMERICAN CYANAMID CO.
XX
XX Jacobsen JS, Vittek MP.
XX WPI; 1998-076482/07.
XX
XX Amyloid precursor protein fusion polypeptides - comprising APP
XX fragment and marker, useful for research and drug screening
XX
XX
XX PS Disclosure; Fig 5A; 84pp; English.
XX
XX The present sequence represents a beta-amyloid peptide (BAP), with
XX a deletion amino acids 11-28 (numbered according to AAM42976). Abnormal
XX accumulation of extracellular BAP in plaques and cerebrovascular
XX deposits is characteristic in brains of individuals suffering from
XX Alzheimers disease and Downs syndrome. BAP is a poorly soluble,
XX self-aggregating protein which is derived from a larger amyloid precursor
XX protein (APP). APP is expressed as an integral membrane protein, and is
XX cleaved by secretase, between BAP 16lys and 17leu. Cleavage at this site
XX precludes amyloidogenesis and results in the release of the
XX amino-terminal APP fragment. Three major isoforms of APP exist: APP-695,
XX APP-751 and APP-770. These isoforms are derived by alternative splicing.
XX APP-APP 751 is a deletion construct of APP-751, which has a deletion of
XX 276 amino acids to within 15 amino acids of the BAP domain. APP can be
XX used as a substrate for studying abnormal proteolytic cleavage which
XX results in the release of BAP, and also to screen for drugs that will
XX inhibit such cleavage.
XX
XX SQ Sequence 45 AA;
XX
XX Query Match 100.0%; Score 54; DB 19; Length 45;
XX Best Local Similarity 100.0%; Pred. No. 0.0012;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
XX
XX AAB37523;
AC
XX
XX 01-MAR-2001 (first entry)
XX
XX Amyloid precursor protein APP residues 669-716.
DE
XX
XX Amyloid precursor protein; APP; Alzheimer's disease; Abeta.
KW
XX
XX Unidentified.
OS
XX
XX W0200066181-A1.
XX
XX 09-NOV-2000.
XX
XX 01-MAY-2000; 2000MO-US11715.
XX
XX 29-APR-1999; 99US-0131579.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Bush AI, Huang X, Atwood CS, Tanzi RE;
XX WPI; 2001-015918/02.
XX
XX Screening for agents useful in treating Alzheimer's disease by adding
XX the agent to an Abeta-containing sample and detecting inhibition of
XX oxygen-dependent hydrogen peroxide formation by the agent.
XX
XX PS Disclosure; Fig 6; 98pp; English.
XX
XX The present invention relates to methods for identifying agents which
XX can be used in the treatment of Alzheimer's disease. These agents are
XX identified for their ability to inhibit oxygen-dependent hydrogen
XX peroxide formation but their inability to inhibit superoxide-dependent
XX hydrogen peroxide formation. This means that they decrease the
XX neurotoxicity of Abeta, the protein which is thought to cause Alzheimer's
XX disease.
XX
XX SQ Sequence 48 AA;
XX
XX Query Match 100.0%; Score 54; DB 22; Length 48;
XX Best Local Similarity 100.0%; Pred. No. 0.0013;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 14
AAB37523
ID AAB37523 standard; peptide; 48 AA.
```

```
XX
XX AAB37523;
AC
XX
XX 01-MAR-2001 (first entry)
XX
XX Amyloid precursor protein APP residues 669-716.
DE
XX
XX Unidentified.
OS
XX
XX W0200066181-A1.
XX
XX 09-NOV-2000.
XX
XX 01-MAY-2000; 2000MO-US11715.
XX
XX 29-APR-1999; 99US-0131579.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Bush AI, Huang X, Atwood CS, Tanzi RE;
XX WPI; 2001-015918/02.
XX
XX Screening for agents useful in treating Alzheimer's disease by adding
XX the agent to an Abeta-containing sample and detecting inhibition of
XX oxygen-dependent hydrogen peroxide formation by the agent.
XX
XX PS Disclosure; Fig 6; 98pp; English.
XX
XX The present invention relates to methods for identifying agents which
XX can be used in the treatment of Alzheimer's disease. These agents are
XX identified for their ability to inhibit oxygen-dependent hydrogen
XX peroxide formation but their inability to inhibit superoxide-dependent
XX hydrogen peroxide formation. This means that they decrease the
XX neurotoxicity of Abeta, the protein which is thought to cause Alzheimer's
XX disease.
XX
XX SQ Sequence 48 AA;
XX
XX Query Match 100.0%; Score 54; DB 22; Length 48;
XX Best Local Similarity 100.0%; Pred. No. 0.0013;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
XX (CEPH-) CEPHALON INC.
PA
XX
XX Howland DS, Scott RW;
PI
XX
XX WPI; 1994-200256/24.
DR
XX
XX Transgenic animal model for Alzheimer's disease - contains
PT transgene encoding amyloid protein under transcriptional control
PT of synapsin gene promoter
XX
XX Example: Page 54; 94pp; English.
PS
XX
XX There was no apparent reference to sequence ID numbers 20, 21 or 22
CC in the specification. The specification describes a transgenic
CC animal model for Alzheimer's disease. A transgenic animal
CC harbouring a transgene coding for an amyloid protein under the
CC control of a promoter is claimed. The amyloid protein can be
CC APP695, APP751 or APP770. The coding sequence may contain a
CC mutation, including the hereditary cerebral haemorrhage with
CC amyloidosis - Dutch type (HCHWA-DT) and familial Alzheimer's
CC disease (FAD). Perhaps SQ IDs 20-22 corresp. to wt. HCHWA-DT
CC and FAD?
CC
XX
XX Sequence 53 AA;
SQ
XX
XX Query Match 100.0%; Score 54; DB 15; Length 53;
XX Best Local Similarity 100.0%; Pred. No. 0.0014;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VKMDAEFRHD 10
Db 2 VKMDAEFRHD 11
1111111111
```

Search completed: October 29, 2002, 10:26:44
Job time : 23.1429 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:36 ; Search time 10.4286 Seconds
(without alignments)
92.140 Million cell updates/sec

Title: US-09-580-018-6

Perfect score: 54

Sequence: 1 VKMDAEFRHD 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	57	2 E60045	Alzheimer's disease
2	54	100.0	57	2 F60045	Alzheimer's disease
3	54	100.0	57	2 G60045	Alzheimer's disease
4	54	100.0	57	2 D60045	Alzheimer's disease
5	54	100.0	57	2 A60045	Alzheimer's disease
6	54	100.0	57	2 B60045	Alzheimer's disease
7	54	100.0	82	2 P00438	Alzheimer's disease
8	54	100.0	693	1 A49795	Alzheimer's disease
9	54	100.0	770	1 QRH044	Alzheimer's disease
10	48	88.9	747	2 JH0773	Alzheimer's disease
11	47	87.0	33	2 S23094	Alzheimer's disease
12	47	87.0	695	2 A27485	Alzheimer's disease
13	47	87.0	695	2 S00550	Alzheimer's disease
14	40	74.1	42	2 PN0512	Alzheimer's disease
15	37	68.5	478	2 C70179	Alzheimer's disease
16	36	66.7	543	2 T48239	Alzheimer's disease
17	36	66.7	578	2 D82053	Alzheimer's disease
18	35	64.8	428	2 B83420	Alzheimer's disease
19	35	64.8	503	2 T24985	Alzheimer's disease
20	35	64.8	511	2 A56750	Alzheimer's disease
21	35	64.8	647	2 T26240	Alzheimer's disease
22	35	64.8	774	2 A81565	Alzheimer's disease
23	35	64.8	900	2 E83189	Alzheimer's disease
24	35	64.8	1001	2 T17365	Alzheimer's disease
25	34	63.0	79	2 D83411	Alzheimer's disease
26	34	63.0	142	2 E89026	Alzheimer's disease
27	34	63.0	213	2 F87669	Alzheimer's disease
28	34	63.0	226	2 T29404	Alzheimer's disease
29	34	63.0	246	2 AG1140	Alzheimer's disease

30	34	63.0	255	2 G90509	dolichol-phosphate
31	34	63.0	376	2 B84277	hypothetical prote
32	34	63.0	400	2 S70187	44.7k vira protein
33	34	63.0	423	2 C84991	elongation factor
34	34	63.0	426	2 B69876	acetylornithine de
35	34	63.0	763	2 JC4376	beta-glucosidase (
36	34	63.0	1237	2 AE1915	hypothetical prote
37	34	63.0	1256	2 AB2042	hypothetical prote
38	33	62.0	293	2 T26934	hypothetical prote
39	33	61.1	177	2 AB3649	hypothetical prote
40	33	61.1	316	2 T46000	hypothetical prote
41	33	61.1	322	2 A69963	hypothetical prote
42	33	61.1	336	2 AF2085	transcription regu
43	33	61.1	392	2 T49471	mucin (muc3) relat
44	33	61.1	427	2 C83591	N-carbamoyl-beta-a
45	33	61.1	811	2 T48468	disease resistance

ALIGNMENTS

RESULT 1
E60045 Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C:Species: Ovis sp. (sheep)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: E60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56130
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 54; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10
DB 3 VKMDAEFRHD 12

RESULT 2
F60045 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: F60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56127; NID:91895; PIDN:CAA39592.1; PID:91896
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 54; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10
DB 3 VKMDAEFRHD 12

```

RESULT 3
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match          100.0%; Score 54; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
   |||||||
DB 3 VKMDAEFRHD 12

RESULT 4
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: D60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56124
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match          100.0%; Score 54; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
   |||||||
DB 3 VKMDAEFRHD 12

RESULT 5
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match          100.0%; Score 54; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 VKMDAEFRHD 10
   |||||||
DB 3 VKMDAEFRHD 12

RESULT 6
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56128; NID:q2165; PID:CAA39593.1; PID:g2166
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match          100.0%; Score 54; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
   |||||||
DB 3 VKMDAEFRHD 12

RESULT 7
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: PQ0438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
A:Reference number: PQ0438; MUID:93075180
A:Accession: PQ0438
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:M83558; GB:M83657
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match          100.0%; Score 54; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
   |||||||
DB 14 VKMDAEFRHD 23

RESULT 8
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991

```


A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a
A:Reference number: A49795; MUID:91273117
A:Accession: A49795
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <PDB>
A:Cross-references: GB:M58727; NID:9342062; PIDN:AAA36829.1; PID:9342063
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing

Query Match 100.0%; Score 54; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMAEPRHD 10
Db 594 VKMAEPRHD 603
|||||

RESULT 9
ORHUA
Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibi
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vasculat
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1987 #sequence revision 28-Jul-1995 #text change 15-Sep-2000
C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A4
4688; A28583; A29302; A60803; J10038; S06121; A60355; A59011; A38384; S29076; S38252; S3
Nucleic Acids Res. 17, 517-522, 1989
A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A:Reference number: S02260; MUID:89128427
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288, 'V', 365-770 <LEM1>
A:Cross-references: EMBL:X13466
A>Note: alternative splice form APP(695)
R:Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
A:Cross-references: EMBL:X13466; NID:935598; PIDN:CAA31830.1; PID:9871360
A>Note: alternative splice form APP(695)
R:La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A:Reference number: A32277; MUID:89165870
A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LAF>
A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AA31654.1; PID:9516074
R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A:Reference number: A33260; MUID:89392030
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <TOH>
A:Cross-references: GB:M29270; NID:9178863; PIDN:AA51768.1; PID:9178865
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A:Reference number: A35486; MUID:90321244
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PRE1>
A>Note: 693-Gln was found in DNA isolated from HCHMA-D patients
R:Ioshikawa, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.

A:Reference number: I39451; MUID:90236318
A:Accession: I39452
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-770 <IOS1>
A:Cross-references: GB:M33112; NID:9178613; PIDN:AA59502.1; PID:9178616
A:Accession: I39451
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-530, 'QWLMPVLPAPFWEAKVGR' <IOS2>
A:Cross-references: GB:M34875; NID:9178608; PIDN:AA59501.1; PID:9178615
R:Yoshikawa, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168
A:Contents: annotation: erratum
A>Note: revised physical map for reference I39451
R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du
Science 248, 1124-1126, 1990
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo
A:Reference number: I39453; MUID:90260663
A:Accession: I39453
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LEV>
A:Cross-references: GB:M37896; NID:9178618; PIDN:AA51727.1; PID:9178620
R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe
A:Reference number: I59562; MUID:92022553
A:Accession: I59562
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUP>
A:Cross-references: GB:S57665; NID:9236720; PIDN:AA31991.1; PID:9236721
R:Kamino, K.; Orr, H.T.; Payant, H.; Wilsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anders
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukulski, W.; Larson, E.; Heston, L.L.; Mart
Am. J. Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t
A:Reference number: A44017; MUID:93053937
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <KAM1>
A:Cross-references: GB:S45135; NID:9257377; PIDN:AA32364.1; PID:9257378
A:Experimental source: familial Alzheimer disease family SB
A>Note: sequence extracted from NCB1 backbone (NCBIP:115374)
A:Accession: B44017
A:Molecule type: DNA
A:Residues: 687-718 <KAM2>
A:Cross-references: GB:S45136; NID:9257379; PIDN:AA32364.1; PID:9257380
A:Experimental source: familial Alzheimer disease family LIT
A>Note: sequence extracted from NCB1 backbone (NCBIP:115376)
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.
Nature 325, 733-736, 1987
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-sur
A:Reference number: A03134; MUID:87144572
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: GB:Y00264; NID:928525; PIDN:CAA68374.1; PID:928526
A>Note: alternative splice form APP(695)
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascula
A:Reference number: A29030; MUID:87231971
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: GB:M16765; NID:9178539; PIDN:AA51722.1; PID:9178540
A>Note: the authors translated the codon GAG for residue 647 as Asp
R:Goldhaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987

A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
 A:Reference number: A47584; MUID:87120328
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756, 'S', 758-770 <GOL>
 A:Cross-references: GB:M15533; NID:9178706; PIDN:AAA5540.1; PID:9178707
 A:Experimental source: brain
 R:Tanzil, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
 Science 235, 880-884, 1987
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
 A:Reference number: A47585; MUID:87120329
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TRAN1>
 A:Cross-references: GB:M15532; NID:9177957; PIDN:AAA51564.1; PID:9177958
 R:Dyck, T.; Weidemann, A.; Mulhapp, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
 EMBO J. 7, 949-957, 1988
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
 A:Reference number: S02638; MUID:88296437
 A:Accession: S02638
 A:Molecule type: mRNA
 A:Residues: 672-678 <DYR>
 R:Tanzil, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Nere
 Nature 331, 528-530, 1988
 A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
 A:Reference number: S00707; MUID:88122640
 A:Accession: S00707
 A:Molecule type: mRNA
 A:Residues: 286-344, 'I', 365-366 <TAN2>
 A:Cross-references: EMBL:X06982; NID:928817; PIDN:CAA30042.1; PID:9292612
 A:Experimental source: promyelocytic leukemia cell line HL60
 A:Note: alternative splice form APP(751)
 R:Porte, P.; Gonzalez-Demnitz, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; De
 Nature 331, 525-527, 1988
 A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
 A:Reference number: S00925; MUID:88122639
 A:Accession: S00925
 A:Molecule type: mRNA
 A:Residues: 1-344, 'I', 365-770 <PO2>
 A:Cross-references: GB:X06989; EMBL:Y00297; NID:928720; PIDN:CAA30050.1; PID:928721
 A:Note: alternative splice form APP(751)
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
 A:Reference number: A38949; MUID:88122641
 A:Accession: A38949
 A:Molecule type: mRNA
 A:Residues: 287-367 <KIT>
 A:Cross-references: GB:X06981; NID:928816; PIDN:CAA30041.1; PID:9292611
 A:Experimental source: glioblastoma cell line
 A:Note: alternative splice form APP(770)
 R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three F
 A:Reference number: A30320
 A:Accession: A30320
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-770 <VIT1>
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 122-288, 'V', 365-770 <VIT2>
 A:Accession: C30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 606-770 <VIT3>
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
 A:Reference number: A31087; MUID:88124954
 A:Accession: A31087
 A:Molecule type: mRNA

A:Residues: 507-770 <ZAI>
 A:Cross-references: GB:M18734; NID:9178572; PIDN:AAA51726.1; PID:9178573
 A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue
 8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue
 A:Note: the cited Genbank accession number, J03594, is not in release 101.0
 R:Masters, C.L.; Mulhapp, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther,
 Query Match 100.0%; Score 54; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.0086;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VKMDAERRHD 10
 |||||
 Db 669 VKMDAERRHD 678
 RESULT 10
 JH0773
 Alzheimer's disease amyloid beta protein precursor - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
 C:Accession: JH0773
 R:Okado, H.; Okamoto, H.
 Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
 A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: development
 A:Reference number: JH0773; MUID:93129227
 A:Accession: JH0773
 A:Molecule type: mRNA
 A:Residues: 1-747 <OKA>
 A:Cross-references: GB:S52417; NID:9263150; PIDN:AAB24853.1; PID:9263151
 A:Experimental source: larva
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinases
 C:Keywords: alternative splicing; amyloid
 F:287-337/Domain: animal kunitz-type proteinase inhibitor homology <BPI>
 Query Match 88.9%; Score 48; DB 2; Length 747;
 Best Local Similarity 80.0%; Pred. No. 0.14;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VKMDAERRHD 10
 |||||
 Db 646 VKMDSEYRHD 655
 RESULT 11
 S23094
 beta-amyloid protein precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
 C:Accession: S23094
 R:Kojima, S.; Omori, M.
 FEBS Lett. 304, 57-60, 1992
 A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic protein
 A:Reference number: S23094; MUID:92316198
 A:Accession: S23094
 A:Molecule type: protein
 A:Residues: 1-33 <KOJ>
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinases
 Query Match 87.0%; Score 47; DB 2; Length 33;
 Best Local Similarity 90.0%; Pred. No. 0.0068;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VKMDAERRHD 10
 |||||
 Db 3 VKMDAERRHD 12
 RESULT 12
 A27485
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
 N:Alternate names: proteinase nexin II
 C:Species: Mus musculus (house mouse)

C>Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
 C:Accession: A27485; S19727; I49485
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.
 Biochem. Biophys. Res. Commun. 149, 615-671, 1987
 A>Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor
 A:Reference number: A27485; MUID:88106489
 A:Accession: A27485
 A:Molecule type: mRNA
 A:Residues: 1-695 <YMA>
 A:Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
 A:Experimental source: brain
 R:de Strooper, B.; van Leuven, F.; van den Berghe, H.
 Blochim. Biophys. Acta 1129, 141-143, 1991
 A>Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
 A:Reference number: S19727; MUID:92096458
 A:Accession: S19727
 A:Molecule type: mRNA
 A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
 A:Cross-references: EMBL:X59379
 R:Izumi, R.; Yamada, T.; Yoshikata, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.
 Gene 112, 189-195, 1992
 A>Title: Positive and negative regulatory elements for the expression of the Alzheimer's
 A:Reference number: I49485; MUID:92209998
 A:Accession: I49485
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-19 <RES>
 A:Cross-references: GB:D10603; NID:g220328; PIDN:BA01456.1; PID:g220329
 C:Genetics:
 A:Map position: 16C3
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 3
 C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 87.0%; Score 47; DB 2; Length 695;
 Best Local Similarity 90.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VKMDAEPFRHD 10
 Db 594 VKMDAEPFRHD 603
 |||||
 S00550

RESULT 13

Alzheimer's disease amyloid beta protein precursor - rat
 N:Alternate names: beta-A4 amyloid protein
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
 C:Accession: S00550; A41245; A39820; S46251
 R:Shivers, B.D.; Hildeich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
 EMBO J. 7, 1365-1370, 1988
 A>Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
 A:Reference number: S00550; MUID:88312583
 A:Accession: S00550
 A:Molecule type: mRNA
 A:Residues: 1-695 <SHI>
 A:Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
 R:Schubert, D.; Schroeder, R.; Lacobriere, M.; Salton, T.; Cole, G.
 Science 241, 223-226, 1988
 A>Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
 A:Reference number: A41245; MUID:88264430
 A:Accession: A41245
 A:Molecule type: protein
 A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
 A>Note: evidence for heparan sulfate attachment
 R:Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.
 FEBS Lett. 349, 109-116, 1994
 A>Title: The beta-A4 amyloid precursor protein binding to copper.
 A:Reference number: S46251; MUID:94320627
 A:Contents: annotation: copper binding sites
 A>Note: rat peptides were isolated but not sequenced
 R:Potempa, A.; Styles, J.; Menta, P.; Kim, K.S.; Miller, D.L.
 J. Biol. Chem. 266, 8464-8469, 1991

A>Title: Purification and tissue level of the beta-amyloid peptide precursor of rat b
 A:Reference number: A39820; MUID:91217087
 A:Accession: A39820
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 18-32 <POT>
 A:Experimental source: brain
 C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
 F:625-648/Domain: transmembrane #status predicted <TMM>

Query Match 87.0%; Score 47; DB 2; Length 695;
 Best Local Similarity 90.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VKMDAEPFRHD 10
 Db 594 VKMDAEPFRHD 603
 |||||
 P00512

RESULT 14

beta-amyloid protein - guinea pig (fragment)
 C:Species: Cavia porcellus (guinea pig)
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
 C:Accession: P00512
 R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Salto, R.; Iwata, T.; Kamiya, H.; Ohno
 Biochem. Biophys. Res. Commun. 193, 624-630, 1993
 A>Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra
 A:Reference number: P00512; MUID:93290653
 A:Accession: P00512
 A:Molecule type: protein
 A:Residues: 1-42 <SHI>
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; amyloid

Query Match 74.1%; Score 40; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 0.23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DAEPFRHD 10
 Db 1 DAEPFRHD 7
 |||||
 C70179

RESULT 15

probable glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - Lyme disease spirochete
 C:Species: Borrelia burgdorferi (Lyme disease spirochete)
 C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 11-Jun-1999
 C:Accession: C70179
 R:Fraser, C.M.; Castjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh
 son, D.; Peterson, J.; Kellavag, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu
 : Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
 Nature 390, 580-586, 1997
 A:Authors: Venter, J.C.
 A>Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
 A:Reference number: A70100; MUID:98065943
 A:Accession: C70179
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-478 <KUE>
 A:Cross-references: GB:AE001165; GB:AE000783; NID:g2688561; PIDN:AAB91531.1; PID:g268
 A:Experimental source: strain B31
 C:Superfamily: glucose-6-phosphate dehydrogenase
 C:Keywords: oxidoreductase

Query Match 68.5%; Score 37; DB 2; Length 478;
 Best Local Similarity 60.0%; Pred. No. 14;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 VKMDAEPFRHD 10

Db : | : | | | |
248 IKFDSERHD 257

Search completed: October 29, 2002, 10:31:04
Job time : 12.4286 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:36 ; Search time 5 Seconds

(without alignments)
77.439 Million cell updates/sec

Title: US-09-580-018-6
Perfect score: 54
Sequence: 1 VKMDAEFRHD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	57	A4_PIG	Q29023 sus scrofa
2	54	100.0	57	A4_URSA	Q29149 ursus marit
3	54	100.0	58	A4_CANFA	Q28280 canis famill
4	54	100.0	58	A4_RABIT	Q28748 oryctolagus
5	54	100.0	58	A4_SHEEP	Q28757 ovis aries
6	54	100.0	59	A4_BOVIN	Q28053 bos taurus
7	54	100.0	751	A4_SAISC	Q95241 salmistr sci
8	54	100.0	770	A4_HUMAN	P05067 homo sapien
9	47	87.0	770	A4_MOUSE	P12033 mus musculu
10	47	87.0	770	A4_RAT	P08592 rattus norv
11	37	68.5	478	G6PD_BOBUB	P01581 bobalia bu
12	35	64.8	511	COPD_BOVIN	P53619 bos taurus
13	35	64.8	511	COPD_HUMAN	P48444 homo sapien
14	35	64.8	900	GLND_PSPAF	Q92980 pseudomonas
15	34	63.0	394	EFTU_BUCAI	Q31257 buchiera ap
16	33	61.1	322	YQJA_BACSU	P54538 bacillus su
17	33	61.1	492	C133_DROME	Q09822 schizosacch
18	33	61.1	927	C133_DROME	Q09822 schizosacch
19	32	59.3	107	T2AH_DROME	Q9W5B9 drosophila
20	32	59.3	132	RNPA_MICLU	P21172 micrococcu
21	32	59.3	198	TNFA_MOUSE	P43468 mus musculu
22	32	59.3	213	NULD_DROME	P32845 drosophila
23	32	59.3	269	T2S1_STRFI	O52512 streptomyc
24	32	59.3	304	MDH_HALMA	Q07841 halocarcu
25	32	59.3	328	P2Y3_MELGA	O93361 melagris g
26	32	59.3	402	RDS1_SCHPO	P53693 schizosacch
27	32	59.3	431	P0R8_SYNPO	P74384 synecocyst
28	32	59.3	500	STCL_EMBNI	Q00707 emeticella
29	32	59.3	502	YGCN_ECOLI	Q46901 escherichia
30	32	59.3	780	TREB_YEAST	P35172 saccharomyc
31	32	59.3	930	DPO1_HABIN	P43741 haemophilus
32	32	59.3	1579	SSK2_YEAST	P53599 saccharomyc
33	31	57.4	77	ACP_BACSU	P80643 bacillus su

34	31	57.4	190	1	GP38_BPSPI	O48394 bacterioph
35	31	57.4	210	1	PEM_MOUSE	P52651 mus musculu
36	31	57.4	351	1	VAOD_HUMAN	P12953 homo sapien
37	31	57.4	351	1	VAOD_MOUSE	P51863 mus musculu
38	31	57.4	453	1	YK8_YEAST	P34252 saccharomyc
39	31	57.4	481	1	THRC_CORGL	P23669 corynebacte
40	31	57.4	497	1	PSD3_SCHPO	Q42897 schizosacch
41	31	57.4	1101	1	KOE5_YEAST	Q08217 saccharomyc
42	31	57.4	1178	1	MNNA_YEAST	P36044 saccharomyc
43	31	57.4	1451	1	A2M2_MOUSE	P28666 mus musculu
44	31	57.4	1476	1	A2M1_MOUSE	P28665 mus musculu
45	31	57.4	1477	1	A113_RAT	P14046 rattus norv

ALIGNMENTS

RESULT 1	ID	A4_PIG	STANDARD:	PRT:	57 AA.
AC	Q29023:				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid				
DE	protein (Beta-APP) (A-beta)] (Fragment).				
GN	APP.				
OS	Sus scrofa (Pig).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.				
ON	NCBI_TaxID=9823;				
RX	SEQUENCE FROM N.A.				
RC	TISSUE=Brain:				
RA	MEDLINE=92017079; PubMed=1656157;				
RT	Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;				
RT	"Conservation of the sequence of the Alzheimer's disease amyloid				
RT	peptide in dog, polar bear and five other mammals by cross-species				
RT	polymerase chain reaction analysis."				
RL	Brain Res. Mol. Brain Res. 10:299-305(1991).				
CC	-1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO				
CC	INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN				
CC	G(O) (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-1- SIMILARITY: BELONGS TO THE APP FAMILY.				
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CC	-----				
DR	EMBL: X56127; CAA39592.1; -.				
DR	HSSP: P05067; IBA4.				
DR	InterPro: IPR001868; A4_APP.				
DR	PROSITE: PS00319; A4_EXTRA; PARTIAL.				
DR	PROSITE: PS00320; A4_INTRA; PARTIAL.				
FW	Glycoprotein; Amyloid; Neurone; Transmembrane.				
FT	NON_TER	1			
FT	CHAIN	6	48		BETA-AMYLOID PROTEIN (POTENTIAL).
FT	DOMAIN	<1	33		EXTRACELLULAR (POTENTIAL).
FT	TRANSEM	34	57		POTENTIAL.
FT	NON_TER	57			
SQ	SEQUENCE	57 AA;	6172 MW;	84209D88EBA82DEA CRC64;	
QY	Query Match	100.0%;	Score 54;	DB 1;	Length 57;
	Best Local Similarity	100.0%;	Pred. No. 0.00024;		
	Matches	10;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

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Db      3 VKMDAEPFRHD 12

RESULT 2
A4_URDMA
ID      A4_URDMA      STANDARD:      PRT:      57 AA.
AC      Q29149;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [contains: Beta-amyloid
DE      protein (Beta-APP) (A-beta)] (Fragment).
GN      APP.
OS      Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX      NCBI_TaxId=29073;

RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      MEDLINE=92017079; PubMed=1656157;
RT      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: X56128; CAA39593.1; -.
DR      HSSP: P05067; 1BA4.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KM      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1      48
FT      CHAIN      6      48      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN      <1      33      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      34      57      POTENTIAL.
FT      NON_TER      57      57
SQ      SEQUENCE      57 AA: 6172 MW: 84209D88BA82DFA CRC64;

Query Match      100.0%; Score 54; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. NO. 0.00024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 VKMDAEPFRHD 10
      |||||
      |||||
Db      3 VKMDAEPFRHD 12

RESULT 3
A4_CANFA
ID      A4_CANFA      STANDARD:      PRT:      58 AA.
AC      Q28280;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [contains: Beta-amyloid
DE      protein (Beta-APP) (A-beta)] (Fragment).
GN      APP.
OS      Canis familiaris (Dog).

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OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX      NCBI_TaxId=9615;

RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Kidney;
RA      MEDLINE=92017079; PubMed=1656157;
RT      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      -----
DR      EMBL: X56125; CAA39590.1; -.
DR      HSSP: P05067; 1BA4.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KM      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1      1
FT      CHAIN      7      49
FT      DOMAIN      <1      34      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      TRANSMEM      35      58      EXTRACELLULAR (POTENTIAL).
FT      NON_TER      58      58      POTENTIAL.
SQ      SEQUENCE      58 AA: 6285 MW: 8469D488A2E12DFA CRC64;

Query Match      100.0%; Score 54; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. NO. 0.00024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 VKMDAEPFRHD 10
      |||||
      |||||
Db      4 VKMDAEPFRHD 13

RESULT 4
A4_RABIT
ID      A4_RABIT      STANDARD:      PRT:      58 AA.
AC      Q28748;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [contains: Beta-amyloid
DE      protein (Beta-APP) (A-beta)] (Fragment).
GN      APP.
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxId=9986;

RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      MEDLINE=92017079; PubMed=1656157;
RT      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

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CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      -----
DR      EMBL: X56129; CAA39594.1; -.
DR      HSSP: P05067; 1BA4.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      CHAIN          1           48      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN         <1        33      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM       34        57      POTENTIAL.
FT      DOMAIN         58        58      CYTOPLASMIC (POTENTIAL).
FT      NON_TER        58
SQ      SEQUENCE      58 AA; 6300 MW; FA34209D88BA82D CRC64;

Query Match          100.0%; Score 54; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VKMDAEFRHD 10
        |||||||
DB      3 VKMDAEFRHD 12

RESULT 5
ID      A4_SHEEP      STANDARD:      PRT:      58 AA.
AC      Q28757;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-Ap) (A-beta)] (Fragment).
GN      APP.
OS      Ovis aries (Sheep).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Caprinae; Ovis.
OX      NCBI_TaxID=9940;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Heart;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
-1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
G(O) (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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DR      EMBL: X56130; CAA39595.1; -.
DR      HSSP: P05067; 1AML.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      CHAIN          1           48      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN         <1        33      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM       34        57      POTENTIAL.
FT      DOMAIN         58        58      CYTOPLASMIC (POTENTIAL).
FT      NON_TER        58
SQ      SEQUENCE      58 AA; 6300 MW; FA34209D88BA82D CRC64;

Query Match          100.0%; Score 54; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VKMDAEFRHD 10
        |||||||
DB      3 VKMDAEFRHD 12

RESULT 6
ID      A4_BOVIN      STANDARD:      PRT:      59 AA.
AC      Q28053;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-Ap) (A-beta)] (Fragment).
GN      APP.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
-1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
G(O) (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      -----
DR      EMBL: X56124; CAA39589.1; -.
DR      EMBL: X56126; CAA39591.1; -.
DR      HSSP: P05067; 1BA4.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      CHAIN          1           49      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN         <1        34      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM       35        58      POTENTIAL.
FT      NON_TER        59
SQ      SEQUENCE      59 AA; 6300 MW; FA34209D88BA82D CRC64;

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FT  NON_TER      59      59      F43469D48A2E12D CRC64;
SQ  SEQUENCE     59 AA;  6414 MW;
Query Match      100.0%; Score 54; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 VKMADEFRHD 10
        |||
        4 VKMADEFRHD 13

RESULT 7
A4_SAISC      STANDARD;      PRT;      751 AA.
ID  A4_SAISC
AC  095241;
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Alzheimer's disease amyloid A4 protein precursor [contains: Beta-
DE  amyloid protein (Beta-APP) (A-beta)].
GN  APP.
OS  Saimiri sciureus (Common squirrel monkey).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX  NCBI_TaxID=9521;
RX  TISSUE=Liver, and Kidney;
RX  MEDLINE=96108492; PubMed=8532114;
RX  Levy E., Amorim A., Frangione B., Walker L.C.;
RT  "beta-amyloid precursor protein gene in squirrel monkeys with
RT  cerebral amyloid angiopathy.";
CC  Neurobiol. Aging 16:805-808(1995).
CC  -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC  INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC  G(O).
CC  -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC  WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC  RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC  NEXT MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC  PHOSPHORYLATION (BY SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC  -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
-----
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DR  EMBL; S81024; AAD14347.1; .
DR  HSSP; P05067; IAAP.
DR  InterPro: IPR001868; A4_APP.
DR  InterPro: IPR002223; Kunitz_BPTI.
DR  Pfam; PF02177; A4_EXTRA; 1.
DR  PRINTS; PR00203; AMYLOIDA4.
DR  PRINTS; PR00759; BASICPTASE.
DR  SMART; SM00006; A4_EXTRA; 1.
DR  SMART; SM00131; KU; 1.
DR  PROSITE; PS00319; A4_EXTRA; 1.
DR  PROSITE; PS00320; A4_INTRA; 1.
DR  PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR  PROSITE; PS00280; BPTI_KUNITZ_2; 1.
DR  PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KM  Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
KM  Signal; Serine protease inhibitor.
FT  SIGNAL      1      17      BY SIMILARITY.
FT  CHAIN      18      751      A4 PROTEIN.
FT  CHAIN      653      695      BETA-AMYLOID PROTEIN (POTENTIAL).

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FT  DOMAIN      18      680      EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM      681      704      POTENTIAL.
FT  DOMAIN      705      751      CYTOPLASMIC (POTENTIAL).
FT  DOMAIN      287      345      BPTI/KUNITZ INHIBITOR.
FT  SITE      740      743      CLATHRIN-BINDING (BY SIMILARITY).
FT  ACT_SITE      301      302      REACTIVE BOND.
FT  DISULFID      291      341      BY SIMILARITY.
FT  DISULFID      300      324      BY SIMILARITY.
FT  DISULFID      316      337      BY SIMILARITY.
FT  CARBOHYD      523      523      N-LINKED (GLCNAC. . .) (PROBABLE).
FT  CARBOHYD      552      552      N-LINKED (GLCNAC. . .) (PROBABLE).
SQ  SEQUENCE     751 AA;  84893 MW;  6C3EA31089569049 CRC64;

Query Match      100.0%; Score 54; DB 1; Length 751;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 VKMADEFRHD 10
        |||
        650 VKMADEFRHD 659

RESULT 8
A4_HUMAN      STANDARD;      PRT;      770 AA.
ID  A4_HUMAN
AC  P05067; P09000; Q16011;
DT  13-AUG-1987 (Rel. 05, Created)
DT  01-NOV-1991 (Rel. 20, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II)
DE  (PN-II) (APP) [contains: Beta-amyloid protein (Beta-APP) (A-beta)].
GN  APP OR A4 OR CVAP OR ADL.
OS  Homo sapiens (Human).
OS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX  NCBI_TaxID=9606;
RX  TISSUE=Brain;
RX  MEDLINE=87144572; PubMed=2881207;
RX  Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RX  Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT  "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT  cell-surface receptor.";
RT  Nature 325:733-736(1987).
RN  [2]
RP  SEQUENCE FROM N.A.
RP  MEDLINE=88122639; PubMed=2893289;
RX  Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RX  Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RX  Cordell B.;
RT  "A new A4 amyloid mRNA contains a domain homologous to serine
RT  proteinase inhibitors.";
RT  Nature 331:525-527(1988).
RN  [3]
RP  SEQUENCE FROM N.A.
RP  MEDLINE=89128427; PubMed=2783775;
RX  Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RX  Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT  "The p7A4(695) precursor protein of Alzheimer's disease A4 amyloid
RT  is encoded by 16 exons.";
RT  Nucleic Acids Res. 17:517-522(1989).
RN  [4]
RP  SEQUENCE FROM N.A.
RP  MEDLINE=97263807; PubMed=9108164;
RX  Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
RX  Saito M., Tsukuni S., Sakaki Y.;
RT  "A novel method for making nested deletions and its application for
RT  sequencing of a 300 kb region of human APP locus.";
RN  [5]
RP  Nucleic Acids Res. 25:1802-1808(1997).
RX  SEQUENCE OF 286-345 AND 365-366 FROM N.A.
RX  MEDLINE=88122640; PubMed=2893290;

```


RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 RN [6]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity.";
 RL Nature 331:530-532(1988).
 RN [7]
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [8]
 RP SEQUENCE OF 507-770 FROM N.A.
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [9]
 RP SEQUENCE OF 672-681.
 RX MEDLINE=88035004; PubMed=3312495;
 RA Pardiidge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tourtelotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels.";
 RL J. Neurochem. 49:1394-1401(1987).
 RN [10]
 RP SEQUENCE OF 739-770 FROM N.A.
 RX MEDLINE=90236318; PubMed=2110105;
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene. 87:257-263(1990).
 RL Gene 87:257-263(1990).
 RN [11]
 RP SEQUENCE OF 1-10 FROM N.A.
 RP TISSUE-Layer:
 RC MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [12]
 RP SEQUENCE OF 18-50.
 RX MEDLINE=87250462; PubMed=3597385;
 RA Van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [13]
 RP IDENTITY OF APP WITH NEXIN-II.
 RX MEDLINE=89384866; PubMed=2506449;
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
 RA Sinha S.;
 RT "The secreted form of the Alzheimer's amyloid precursor protein with
 RT the kunitz domain is protease nexin-II.";
 RL Nature 341:144-147(1989).
 RN [14]
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RX MEDLINE=90211252; PubMed=1969731;
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Corell B., Katunuma N.;
 RT "Protease-specificity of kunitz inhibitor domain of Alzheimer's
 RT disease amyloid protein precursor.";

RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
 RN [15]
 RP COMPLEX WITH G(O).
 RX MEDLINE=93188965; PubMed=8446172;
 RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
 RA Murayama Y., Ogata E.;
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 RT protein G(O).";
 RL Nature 362:75-79(1993).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
 RX MEDLINE=99215582; PubMed=10201399;
 RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinsty W.J.,
 RA Galatis D., Heese L., Multhaup G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RT "Crystal structure of the N-terminal, growth factor-like domain of
 RT Alzheimer amyloid precursor protein.";
 RL Nat. Struct. Biol. 6:327-331(1999).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
 RX MEDLINE=91104913; PubMed=2125487;
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kosiakof A.A.;
 RT "X-ray crystal structure of the protease inhibitor domain of
 RT Alzheimer's amyloid beta-protein precursor.";
 RL Biochemistry 29:10018-10022(1990).
 RN [18]
 RP STRUCTURE BY NMR OF 289-344.
 RX MEDLINE=92031488; PubMed=1718421;
 RA Heald S.L., Tilton R.F., Jr., Hammond L.S., Lee A., Bayney R.M.,
 RA Kamaeck M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterebeck A.,
 RA Tamburini P.P.;
 RT "Sequential NMR resonance assignment and structure determination of
 RT the kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
 RT precursor protein.";
 RL Biochemistry 30:10467-10476(1991).
 RN [19]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=94281210; PubMed=7516706;
 RA Talafous J., Marchynski K.J., Klopman G., Zagorski M.G.;
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
 RL Biochemistry 33:7788-7796(1994).
 RN [20]
 RP STRUCTURE BY NMR OF 696-706.
 RX MEDLINE=97128622; PubMed=8973180;
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
 RT membrane-mimicking environment.";
 RL Biochemistry 35:16094-16104(1996).
 RN [21]
 RP STRUCTURE BY NMR OF 672-711.
 RX MEDLINE=98359783; PubMed=9693002;
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscelle
 RT environment. Is the membrane-spanning domain where we think it is?";
 RL Biochemistry 37:11064-11077(1998).
 RN [22]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=20400066; PubMed=10940222;
 RA Poulsen S.-A., Watson A.A., Craik D.J.;
 RT "Solution structures in aqueous SDS micelles of two amyloid beta
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
 RT site.";
 RL J. Struct. Biol. 130:142-152(2000).
 RN [23]
 RP STRUCTURE BY NMR OF 681-706.
 RX MEDLINE=20400065; PubMed=10940221;
 RA Zhang S., Iwata K., Lachenmann M.J., Peng J.W., Li S., Stimson E.R.,
 RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;
 RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in
 RT water.";
 RL J. Struct. Biol. 130:130-141(2000).
 RN [24]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.

DB 669 VKMDAEFGHD 678

RESULT 10

AC A4_RAT STANDARD: PRT: 770 AA.

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog precursor (Amyloidogenic glycoprotein) (AG).

GN APP

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_Taxid=10116;

RP [1]

RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.

RC TISSUE=Brain;

RC MEDLINE=88312583; PubMed=2900758;

RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K., Seeburg P.H.;

RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.";

RT EMBO J. 7:1365-1370(1988).

RN [2]

RP SEQUENCE OF 289-364 FROM N.A.

RC TISSUE=Liver;

RC MEDLINE=89183625; PubMed=2648331;

RA Kang J., Mueller-Hill B.;

RT "The sequence of the two extra exons in rat preA4.";

RC Nucleic Acids Res. 17:2130-2130(1989).

CL -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695), APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11 ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.

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CC -----

DR EMBL: X07648; CAA30488.1; -

DR EMBL: X14066; CAA32229.1; -

DR PIR: S00550; S00550.

DR PIR: S03607; S03607.

DR HSSP: P05067; IAAP.

DR InterPro: IPR001868; A4_APP.

DR InterPro: IPR002223; Kunitz_BPTI.

DR Pfam: PF02177; A4_EXTRA.1.

DR Pfam: PF00014; Kunitz_BPTI.1.

DR PRINTS: PR00203; AMYLOD4.

DR PRINTS: PR00759; BASICPTASE.

DR SMART: SM00006; A4_EXTRA.1.

DR SMART: SM00131; KU.1.

DR PROSITE: PS00319; A4_EXTRA.1.

DR PROSITE: PS00320; A4_INTRA.1.

DR PROSITE: PS00280; BPTI_KUNITZ_1.

DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.

DR Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;

KW Alternative splicing; Serine protease inhibitor.

FT SIGNAL 1 17 BY SIMILARITY.

FT CHAIN 18 770 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN

FT DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 700 723 POTENTIAL.

FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 673 715 EQUIVALENT OF BETA-AMYLOID PROTEIN.

FT SITE 287 345 BPTI/KUNITZ INHIBITOR.

FT SITE 759 762 CLATHRIN-BINDING (BY SIMILARITY).

FT DISULFD 291 341 BY SIMILARITY.

FT DISULFD 300 324 BY SIMILARITY.

FT DISULFD 316 337 BY SIMILARITY.

FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPIC 289 289 E -> V (IN ISOFORM APP(695)).

FT VARSPIC 290 364 MISSING (IN ISOFORM APP(695)).

SO SEQUENCE 770 AA; 86704 MW; C26C9DBB2D929A7 CRC64;

Query Match 87.0%; Score 47; DB 1; Length 770;

Best Local Similarity 90.0%; Pred. No. 0.092;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VKMDAEFGHD 10

DB 669 VKMDAEFGHD 678

RESULT 11

G6PD_BORBU

ID G6PD_BORBU STANDARD: PRT: 478 AA.

AC 051581;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD).

GN ZNF OR B06536.

OS Borrelia burgdorferi (Lyme disease spirochete).

OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.

OX NCBI_Taxid=139;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 35210 / B31;

RC MEDLINE=98065943; PubMed=9403685;

RA Fraser C.M., Casjens S., Huang W.M., Dodson R., Hickey E.K., Gwin M., Lathigra R., White O., Ketchum K.A.,

RA Dougerson J., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kellaway A.R., Quackenbush J., Salzberg S., Hanson M., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Uterback T., Wathey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.;

RT "Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.";

RT Nature 390:580-586(1997).

RT NATURE 390:580-586(1997).

CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D-glucono-1,5-lactone 6-phosphate + NADPH.

CC -1- PATHWAY: FIRST STEP IN PENTOSE PHOSPHATE PATHWAY.

CC -1- SIMILARITY: BELONGS TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE FAMILY.

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CC -----

DR EMBL: AE001165; AAB91531.1; -

DR HSSP: P11411; IDPG.

DR TIGR: BB0636; -

DR InterPro: IPR001282; G6PD.

DR Pfam: PF00479; G6PD.1.

DR Pfam: PF02781; G6PD_C; 1.

```
DR PRINTS: PR00079; G6PDHHRGNASE.
DR PRODOM: PD001129; G6PD; 1.
DR PROSITE: PS00069; G6P_DEHYDROGENASE; 1.
KW Oxidoreductase; NADP; Glucose metabolism; Complete proteome.
FT ACT_SITE 176 176 BY SIMILARITY.
SQ SEQUENCE 478 AA; 56113 MW; 4DDCE2861161C8A CRC64;

Query Match          68.5%; Score 37; DB 1; Length 478;
Best Local Similarity 60.0%; Pred. No. 5.6;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKMDAERHHD 10
   :|:|:|
Db 248 IKFDESEFHD 257

RESULT 12
COPD_BOVIN STANDARD: PRT; 511 AA.
ID COPD_BOVIN
AC P53619;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coatomer delta subunit (Delta-coat protein) (Delta-COP).
GN COPD.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 2-511 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97011152; PubMed=8858162;
RA Falstich D., Auerbach S., Orci L., Ravazzola M., Wegehingel S.,
RA Lottspeich F., Stenbeck G., Harter C., Wieland F.T., Tschöner H.;
RT "Architecture of coatomer: molecular characterization of delta-COP
RT and protein interactions within the complex.";
RL J. Cell Biol. 135:53-61(1996).
CC -1- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS
CC TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-
CC CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC
CC PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI
CC NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI
CC MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER
CC TRANSPORT OF DILYSINE-TAGGED PROTEINS. IN MAMMALS, THE COATOMER
CC CAN ONLY BE RECRUITED BY MEMBRANES ASSOCIATED TO ADP-RIBOSYLATION
CC FACTORS (ARFS), WHICH ARE SMALL GTP-BINDING PROTEINS. THE COMPLEX
CC ALSO INFLUENCES THE GOLGI STRUCTURAL INTEGRITY, AS WELL AS THE
CC PROCESSING, ACTIVITY, AND ENDOCYTIC RECYCLING OF LDL RECEPTORS (BY
CC SIMILARITY).
CC -1- SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA,
CC BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.
CC -1- SUBCELLULAR LOCATION: THE COATOMER IS CYTOPLASMIC OR POLYMERIZED
CC ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE
CC VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: UBICITOUSLY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
CC FAMILY. COPD SUBFAMILY.
CC -----
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CC -----
DR EMBL: X94265; CAA63941.1; -.
DR InterPro: IPR001392; Adap_comp_sub.
DR Pfam: PF00928; Adap_comp_sub; 1.
KW Transport; Protein transport; Golgi stack; Membrane.
SQ SEQUENCE 511 AA; 57274 MW; 6A285798F252CCTF CRC64;
```

```
Query Match          64.8%; Score 35; DB 1; Length 511;
Best Local Similarity 55.6%; Pred. No. 15;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KMDAERHHD 10
   :|:|:|
Db 424 EIDGEXRHD 432

RESULT 13
COPD_HUMAN STANDARD: PRT; 511 AA.
ID COPD_HUMAN
AC P48444;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coatomer delta subunit (Delta-coat protein) (Delta-COP) (Archain).
GN COPD OR ARCNI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95301274; PubMed=7782067;
RA Radice P., Pensotti V., Jones C., Perry H., Pierotti M.A.,
RA Tunaciliffe A.;
RT "The human archain gene, ARCNI, has highly conserved homologs in rice
RT and Drosophila.";
RL Genomics 26:101-106(1995).
CC -1- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS
CC TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-
CC CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC
CC PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI
CC NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI
CC MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER
CC TRANSPORT OF DILYSINE-TAGGED PROTEINS. IN MAMMALS, THE COATOMER
CC CAN ONLY BE RECRUITED BY MEMBRANES ASSOCIATED TO ADP-RIBOSYLATION
CC FACTORS (ARFS), WHICH ARE SMALL GTP-BINDING PROTEINS. THE COMPLEX
CC ALSO INFLUENCES THE GOLGI STRUCTURAL INTEGRITY, AS WELL AS THE
CC PROCESSING, ACTIVITY, AND ENDOCYTIC RECYCLING OF LDL RECEPTORS (BY
CC SIMILARITY).
CC -1- SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA,
CC BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.
CC -1- SUBCELLULAR LOCATION: THE COATOMER IS CYTOPLASMIC OR POLYMERIZED
CC ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE
CC VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: UBICITOUSLY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
CC FAMILY. COPD SUBFAMILY.
CC -----
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CC -----
DR EMBL: X81197; CAA57071.1; -.
DR EMBL: X81198; CAA57072.1; ALT_INIT.
DR MIM: 600820; -.
DR InterPro: IPR001392; Adap_comp_sub.
DR Pfam: PF00928; Adap_comp_sub; 1.
KW Transport; Protein transport; Golgi stack; Membrane; Polymorphism.
FT VARIANT 186 186 F->L (IN DBSNP:682327).
FT VARIANT 309 309 /FTID-VAR_011789.
FT FTID-VAR_011789.
FT K->N (IN DBSNP:1063124).
FT FTID-VAR_011789.
SQ SEQUENCE 511 AA; 57210 MW; 4ED1F7D2D12A7E75 CRC64;

Query Match          64.8%; Score 35; DB 1; Length 511;
```

Best Local Similarity 55.6%; Pred. No. 15;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KMDAEFRH 10
Db 424 EIDGEXRHD 432

RESULT 14

GIND_PSEAE STANDARD; PRT; 900 AA.

AC Q929H0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE [Protein-PilI uridylyltransferase (EC 2.7.7.59) (Pti uridylyl-
transferase) (uridylyl removing enzyme) (Urase)].
GN GIND OR PA3658.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RA Nishimoto H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
Hickey M.J., Britman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Lartig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Kaiser J., Sater W.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -1- FUNCTION: MODIFIES, BY URIDYLYLATION OR DEURIDYLYLATION THE PII
(GLNB) REGULATORY PROTEIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: UTP + [protein-PilI] = diphosphate + uridylyl-
[protein-PilI].
CC -1- SIMILARITY: BELONGS TO THE GIND FAMILY.
CC -1- CAUTION: REF.1 DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN
POSITION 285.

CC -----
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CC -----

DR EMBL: AB024601; BAA75913.1; ALT_FRAME.
DR EMBL: AE004785; AAG07046.1; -.
DR InterPro: IPR002912; ACT.
DR InterPro: IPR002819; HD.
DR InterPro: IPR003607; HDC.
DR InterPro: IPR002934; NTP_transf.
DR Pfam: PF01842; ACT; 2.
DR Pfam: PF01842; HD; 1.
DR Pfam: PF01909; NTP_transf_2; 1.
DR SMART: SM00471; HDC; 1.
KM Transferrase: Nucleotidyltransferase; Complete proteome.
FT CONFLICT 811 811 L->V (IN REF. 1).
SQ SEQUENCE 900 AA: 103404 MW: 7071F31EC284E836 CR664;

Query Match 64.8%; Score 35; DB 1; Length 900;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 MDAEFRH 10
Db 400 IDDEFRH 407

RESULT 15

EFTU_BUCAI STANDARD; PRT; 394 AA.

AC Q31297;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Elongation factor Tu (EF-Tu).
GN TUF OR B0526.
OS Bacillus subtilis (subsp. *Acetobacterium*) (Acetobacterium pium
symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=116099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TOKYO 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
RL Nature 407:81-86(2000).
RN [2]
RP SEQUENCE OF 20-384 FROM N.A.
RX MEDLINE=98242088; PubMed=9580987;
RA Brynne E.U., Kurland C.G., Moran N.A., Andersson S.G.;
RT "Evolutionary rates for tuf genes in endosymbionts of aphids.";
RL Mol. Biol. Evol. 15:574-582(1998).
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
CC AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
CC BIOSYNTHESIS.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-TU/EF-1A SUBFAMILY.

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CC -----

DR EMBL: AF001119; BAB13219.1; ALT_INIT.
DR EMBL: Y12307; CAA72974.1; -.
DR HSP: P02990; LEU.
DR InterPro: IPR000795; GTP_EFTU.
DR Pfam: PF00009; GTP_EFTU; 1.
DR PRINTS: PR00315; ELONGACTNFCY.
DR PROSITE: PS00301; EFACFOR_GTP; 1.
KM Elongation factor; Protein biosynthesis; GTP-binding;
KW Complete proteome.
FT NP BIND 19 26 GTP (BY SIMILARITY).
FT NP BIND 81 85 GTP (BY SIMILARITY).
FT NP BIND 136 139 GTP (BY SIMILARITY).
FT CONFLICT 89 89 I->M (IN REF. 2).
SQ SEQUENCE 394 AA: 43465 MW: 09B73EADCA0DF5F6 CR664;

Query Match 63.0%; Score 34; DB 1; Length 394;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKMDAEFRH 9
Db 68 VEYDFEFRH 76

Tue Oct 29 11:23:38 2002

us-09-580-018-6.rsp

Page 10

Search completed: October 29, 2002, 10:27:31
Job time : 6 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:11 ; Search time 18 seconds

(without alignments)
96.108 Million cell updates/sec

Title: US-09-580-018-6
Perfect score: 54
Sequence: 1 VKMADEFRRD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_19:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*
15: sp.rvivirus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	82	4 P78438	P78438 homo sapien
2	54	100.0	82	4 Q16014	Q16014 homo sapien
3	54	100.0	82	4 Q16019	Q16019 homo sapien
4	54	100.0	82	4 Q16020	Q16020 homo sapien
5	54	100.0	534	13 Q93296	Q93296 gallus galli
6	54	100.0	569	13 Q9PVL1	Q9PVL1 gallus galli
7	54	100.0	695	6 Q95KN7	Q95KN7 macaca fasc
8	54	100.0	695	11 Q60496	Q60496 cavia sp. P
9	54	100.0	695	13 Q9DGB8	Q9DGB8 gallus galli
10	54	100.0	751	13 Q9DGB7	Q9DGB7 gallus galli
11	54	100.0	770	6 Q9TUI0	Q9TUI0 sus scrofa
12	48	88.9	693	13 Q98SG0	Q98SG0 xenopus lae
13	48	88.9	693	13 Q98SF9	Q98SF9 xenopus lae
14	48	88.9	747	13 Q91963	Q91963 xenopus. ap
15	47	87.0	79	11 Q35463	Q35463 cricetus
16	47	87.0	607	11 Q99K32	Q99K32 mus musculu

17	47	87.0	695	11 P97487	P97487 mus musculu
18	41	75.9	423	2 O52379	O52379 raietonia s
19	41	75.9	423	2 O45693	O45693 burkholderi
20	40	74.1	19	4 Q9UCB8	Q9UCB8 homo sapien
21	40	74.1	28	4 Q9UCD1	Q9UCD1 homo sapien
22	40	74.1	30	4 Q9UCB9	Q9UCB9 homo sapien
23	40	74.1	33	4 Q9UCB3	Q9UCB3 homo sapien
24	37	68.5	210	2 Q93MK6	Q93MK6 vibrio vuln
25	37	68.5	329	17 Q9HMG1	Q9HMG1 halobacteri
26	36	66.7	543	10 Q9LZL4	Q9LZL4 arabidopsis
27	36	66.7	578	16 Q9KNV0	Q9KNV0 vibrio chol
28	36	66.7	755	5 Q9VFE30	Q9VFE30 drosophila
29	35	64.8	347	12 Q91ED6	Q91ED6 chilo iride
30	35	64.8	428	16 Q91Z04	Q91Z04 pseudomonas
31	35	64.8	454	5 Q9UA07	Q9UA07 caenorhabdi
32	35	64.8	462	5 Q9Y198	Q9Y198 caenorhabdi
33	35	64.8	473	11 Q91VGT	Q91VGT mus musculu
34	35	64.8	475	5 Q9U343	Q9U343 caenorhabdi
35	35	64.8	503	5 Q21424	Q21424 caenorhabdi
36	35	64.8	511	11 Q91W48	Q91W48 mus musculu
37	35	64.8	634	5 Q9U9Y8	Q9U9Y8 caenorhabdi
38	35	64.8	747	5 Q62395	Q62395 caenorhabdi
39	35	64.8	774	16 Q92CV7	Q92CV7 listeria in
40	35	64.8	1001	4 Q9H2K7	Q9H2K7 homo sapien
41	35	64.8	1001	4 Q96175	Q96175 homo sapien
42	35	64.8	1001	11 Q98664	Q98664 rattus norv
43	35	64.8	1005	4 Q9P216	Q9P216 homo sapien
44	34	63.0	79	16 Q52658	Q52658 pseudomonas
45	34	63.0	105	10 Q91LJ9	Q91LJ9 pyrus pyrif

ALIGNMENTS

RESULT 1
P78438 PRELIMINARY; PRT; 82 AA.
AC P78438;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).
GN App.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8932030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [2]
RP SEQUENCE OF 19-48 FROM N.A.
RX MEDLINE=87120329; PubMed=2949367;
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Nave R.L.;
RT "Amyloid beta protein gene: CDNA, mRNA distribution, and genetic
RT linkage near the Alzheimer locus.";
RL Science 235:880-884(1987).
RN [3]
RP SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE=93035397; PubMed=1415269;
RA Kurland K., Orr H.T., Payami H., Wilsman E.M., Alonso M.E., Pulst S.M.,
RA Anderson L., O'dahl S., Nemens E., White J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease
RT kindreds for the APP gene region.";
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL; M29270; AAA51768.1; -
DR EMBL; M29269; AAA51768.1; JOINED.

DR EMBL: M15532: AAA51564.1; -;
 DR EMBL: S45136: AAB23646.1; -;
 DR HSSP: P05067; 1BA4.
 FT NON_TER 1
 SQ SEQUENCE 82 AA; 8994 MW; 8DA9EA2B813A070E CRC64;

Query Match 100.0%; Score 54; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 0.0019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10
 DB 14 VKMDAEFRHD 23

RESULT 2

O16014 PRELIMINARY; PRT; 82 AA.

AC O16014; 01-NOV-1996 (TREMBLREL. 01, Created)
 DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)
 DE BETA-AMYLOID PEPTIDE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93236601; PubMed=8476439;
 RA Denman R.B., Rosenzweig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 DR EMBL: S60721; AAB26263.2; -;
 DR HSSP: P05067; 1BA4.
 FT NON_TER 1
 FT NON_TER 82
 SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 54; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 0.0019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10
 DB 15 VKMDAEFRHD 24

RESULT 3

O16019 PRELIMINARY; PRT; 82 AA.

AC O16019; 01-NOV-1996 (TREMBLREL. 01, Created)
 DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)
 DE BETA-AMYLOID PEPTIDE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93236601; PubMed=8476439;
 RA Denman R.B., Rosenzweig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 DR EMBL: S61380; AAB26264.2; -;
 DR HSSP: P05067; 1BA4.
 FT NON_TER 1
 FT NON_TER 82

SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 100.0%; Score 54; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 0.0019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10
 DB 15 VKMDAEFRHD 24

RESULT 4

O16020 PRELIMINARY; PRT; 82 AA.

AC O16020; 01-NOV-1996 (TREMBLREL. 01, Created)
 DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)
 DE BETA-AMYLOID PEPTIDE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93236601; PubMed=8476439;
 RA Denman R.B., Rosenzweig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 DR EMBL: S61383; AAB26265.2; -;
 DR HSSP: P05067; 1BA4.
 FT NON_TER 1
 FT NON_TER 82
 SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 100.0%; Score 54; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 0.0019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10
 DB 15 VKMDAEFRHD 24

RESULT 5

O93296 PRELIMINARY; PRT; 534 AA.

AC O93296; 01-NOV-1998 (TREMBLREL. 08, Created)
 DT 01-NOV-1998 (TREMBLREL. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)
 DE AMYLOID PROTEIN (FRAGMENT).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98337885; PubMed=9671674;
 RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
 RA Milligan C.E.;
 RT "Increased production of amyloid precursor protein provides a
 substrate for caspase-3 in dying motoneurons.";
 J. Neurosci. 18:5869-5880(1998).
 DR EMBL: AF042098; AAC25052.1; -;
 DR HSSP: P05067; 1BA4.
 DR InterPro: IPR001868; A4_APP.
 DR PRINTS: PR00203; AMYLOID4.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.


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FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53EC2E66D4C92 CRC64;
Query Match 100.0%; Score 54; DB 13; Length 534;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10
Db 433 VKMDAEFRHD 442

RESULT 6
O95KNT PRELIMINARY; PRT; 569 AA.
ID O95KNT
AC O95KNT
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Coulson E.J., Paliaga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function."
RL Neurochem. Int. 0:0-0(2000).
DR EMBL: AF030341; AAF12698.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;
Query Match 100.0%; Score 54; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10
Db 469 VKMDAEFRHD 478

RESULT 7
O95KNT PRELIMINARY; PRT; 695 AA.
ID O95KNT
AC O95KNT
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AMYLOID B-PROTEIN PRECURSOR.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RX MEDLINE-91273117; PubMed-1905108;
RA Podlasy M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's

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RT disease."
RL Am. J. Pathol. 138:1423-1435(1991).
DR EMBL: M58727; AAA36829.1; -.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 597 636 POTENTIAL.
SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;
Query Match 100.0%; Score 54; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10
Db 594 VKMDAEFRHD 603

RESULT 8
O60496 PRELIMINARY; PRT; 695 AA.
ID O60496
AC O60496
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE AMYLOID PRECURSOR PROTEIN.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE-97236426; PubMed-9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing."
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL: X97631; CA66230.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;
Query Match 100.0%; Score 54; DB 11; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VKMDAEFRHD 10
Db 594 VKMDAEFRHD 603

RESULT 9
O9DGJ8 PRELIMINARY; PRT; 695 AA.
ID O9DGJ8
AC O9DGJ8
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolase A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms."

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RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289218; AAC00593.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match
Best Local Similarity 100.0%; Score 54; DB 13; Length 695;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
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Db 594 VKMDAEFRHD 603

RESULT 10
Q9DGJ7 PRELIMINARY; PRT; 751 AA.
AC Q9DGJ7;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolosse A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
   isoforms."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289219; AAC00594.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match
Best Local Similarity 100.0%; Score 54; DB 13; Length 751;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
   |||||
Db 650 VKMDAEFRHD 659

RESULT 11
Q9TUI0 PRELIMINARY; PRT; 770 AA.
AC Q9TUI0;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

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OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid Precursor Protein 770."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB032550; BAA84580.1; -.
DR HSSP: P05067; 1AAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BC583E CRC64;

Query Match
Best Local Similarity 100.0%; Score 54; DB 6; Length 770;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
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Db 669 VKMDAEFRHD 678

RESULT 12
Q98SG0 PRELIMINARY; PRT; 693 AA.
ID Q98SG0;
AC Q98SG0;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN A.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RT Thesis (2001). Department of Biological Sciences,
   University of Nijmegen, Nijmegen, Netherlands.
RL EMBL: AJ298150; CAC37193.1; -.
DR HSSP: P05067; 1H23.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
KW Signal.
FT SIGNAL 1 18 POTENTIAL.
SQ SEQUENCE 693 AA; 78568 MW; CAF1DF655C1AB653 CRC64;

Query Match
Best Local Similarity 88.9%; Score 48; DB 13; Length 693;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
   |||||
Db 592 VKMDSEYRHD 601

RESULT 13

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Q98SF9
ID Q98SF9 PRELIMINARY; PRT; 695 AA.
AC Q98SF9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN B.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
University of Nijmegen, Nijmegen, Netherlands.
DR EMBL; AJ296151; CAC37194.1; -.
DR HSSP; P05067; 1H23.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00066; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 695 AA; 78803 MW; DC4EB02AFB0204A CRC64;

Query Match
Best Local Similarity 88.9%; Score 48; DB 13; Length 695;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
|1111111111|
Db 594 VKMDSYRHD 603

RESULT 14
Q91963 PRELIMINARY; PRT; 747 AA.
AC Q91963;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE APP747.
GN APP747.
OS Xenopus.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae.
OX NCBI_TaxID=8353;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93129227; PubMed=1282805;
RA Okado H., Okamoto H.;
RT "A Xenopus homologue of the human beta-amyloid precursor protein:
RT developmental regulation of its gene expression";
RT Biochem Biophys Res Commun. 189:1561-1568(1992).
DR EMBL; S52417; AAB24853.1; -.
DR HSSP; P05067; 1H23.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00066; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

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DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 747 AA; 84893 MW; A75E81885681D948 CRC64;

Query Match
Best Local Similarity 88.9%; Score 48; DB 13; Length 747;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
|1111111111|
Db 646 VKMDSYRHD 655

RESULT 15
Q35463 PRELIMINARY; PRT; 79 AA.
AC Q35463;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).
GN BETA APP.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Sambamurti K., Pimlx I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF030413; AAB86608.1; -.
DR HSSP; P05067; 1BA4.
FT NON_TER 1
FT NON_TER 79
FT NON_TER 79
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match
Best Local Similarity 87.0%; Score 47; DB 11; Length 79;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
|1111111111|
Db 18 VKMDAEFRGHD 27

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Search completed: October 29, 2002, 10:29:43
 Job time : 19.1429 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:56 ; Search time 9 Seconds
(without alignments)
27.140 Million cell updates/sec

Title: US-09-580-018-6

Perfect score: 54

Sequence: 1 VKMDAEFRMD 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCRMUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	16	5	PCT-US94-07043A-1
2	54	100.0	18	2	US-08-149-975A-3
3	54	100.0	27	1	US-08-141-32A-11
4	54	100.0	27	1	US-08-541-902-11
5	54	100.0	45	1	US-08-462-859A-5
6	54	100.0	45	1	US-08-123-659A-5
7	54	100.0	45	1	US-08-464-247A-5
8	54	100.0	45	1	US-08-464-248A-5
9	54	100.0	53	4	US-09-173-887-5
10	54	100.0	58	1	US-08-371-930-25
11	54	100.0	58	5	PCT-US94-01712-25
12	54	100.0	59	1	US-08-484-969-3
13	54	100.0	59	1	US-08-472-627-3
14	54	100.0	59	1	US-08-388-463-3
15	54	100.0	63	1	US-08-462-859A-3
16	54	100.0	63	1	US-08-462-859A-4
17	54	100.0	63	1	US-08-123-659A-3
18	54	100.0	63	1	US-08-123-659A-4
19	54	100.0	63	1	US-08-464-247A-3
20	54	100.0	63	1	US-08-464-247A-4
21	54	100.0	63	1	US-08-464-248A-3
22	54	100.0	63	1	US-08-464-248A-4
23	54	100.0	103	2	US-08-404-831-2
24	54	100.0	103	2	US-08-612-785B-2
25	54	100.0	103	2	US-08-475-579A-2
26	54	100.0	103	2	US-08-920-162A-2
27	54	100.0	103	3	US-08-339-708A-10

28	54	100.0	103	4	US-09-356-931-2	Sequence 2, Appl1
29	54	100.0	103	4	US-08-703-675C-2	Sequence 2, Appl1
30	54	100.0	103	4	US-08-617-267C-2	Sequence 2, Appl1
31	54	100.0	105	2	US-08-729-345-1	Sequence 1, Appl1
32	54	100.0	117	2	US-08-729-345-3	Sequence 3, Appl1
33	54	100.0	152	6	5187153-4	Patent No. 5187153
34	54	100.0	162	6	5220013-4	Patent No. 5220013
35	54	100.0	162	6	5223482-4	Patent No. 5223482
36	54	100.0	264	1	US-07-990-893-5	Sequence 5, Appl1
37	54	100.0	487	1	US-08-462-859A-9	Sequence 9, Appl1
38	54	100.0	487	1	US-08-123-659A-9	Sequence 9, Appl1
39	54	100.0	487	1	US-08-464-247A-9	Sequence 9, Appl1
40	54	100.0	487	1	US-08-464-248A-9	Sequence 9, Appl1
41	54	100.0	492	1	US-08-462-859A-7	Sequence 7, Appl1
42	54	100.0	492	1	US-08-123-659A-7	Sequence 7, Appl1
43	54	100.0	492	1	US-08-464-247A-7	Sequence 7, Appl1
44	54	100.0	492	1	US-08-464-248A-7	Sequence 7, Appl1
45	54	100.0	537	1	US-08-453-552-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
PCT-US94-07043A-1
Sequence 1, Application PC/TUS9407043A
GENERAL INFORMATION:
APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,
APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard
TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC
TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Miles Inc.
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
COMPUTER: Sharp PC 4600
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07043A
FILING DATE: June 21, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10889
FILING DATE: November 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/995,660
FILING DATE: December 16, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/880,914
FILING DATE: May 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Pamela A. Simonton
REGISTRATION NUMBER: 31,060
REFERENCE/DOCKET NUMBER: MTI 224.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 937-2340
TELEFAX: (203) 937-2795
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-07043A-1
Query Match 100.0%; Score 54; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00011;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
|||||
Db 4 VKMDAEFRHD 13

RESULT 2

US-08-149-975A-3

; Sequence 3, Application US/08149975A
; Patent No. 5849600

GENERAL INFORMATION:

APPLICANT: Nixon, Ralph

APPLICANT: Honda, Toshiyuki

TITLE OF INVENTION: DIAGNOSTIC ASSAYS FOR ALZHEIMER'S

TITLE OF INVENTION: DISEASE

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/149,975A

FILING DATE: 11-NOV-1993

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 04843/016001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-149-975A-3

QY 1 VKMDAEFRHD 10

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Db 1 VKMDAEFRHD 10

Query Match 100.0%; Score 54; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

US-08-141-324-11

; Sequence 11, Application US/08141324

; Patent No. 5475097

GENERAL INFORMATION:

APPLICANT: Travis, James

APPLICANT: Potempa, Jan S.

APPLICANT: Barr, Philip J.

APPLICANT: Pavloff, Nadine

APPLICANT: Pike, Robert N.

TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis

TITLE OF INVENTION: Protease

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201

CITY: Boulder

STATE: CO

COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/141,324

FILING DATE: 21-OCT-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Ferber, Donna M.

REGISTRATION NUMBER: 33,878

REFERENCE/DOCKET NUMBER: 44-93

TELECOMMUNICATION INFORMATION:

TELEPHONE: 303-499-8080

TELEFAX: 303-499-8089

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-141-324-11

QY 1 VKMDAEFRHD 10

|||||
Db 6 VKMDAEFRHD 15

Query Match 100.0%; Score 54; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4

US-08-541-902-11

; Sequence 11, Application US/08541902

; Patent No. 5707620

GENERAL INFORMATION:

APPLICANT: Travis, James

APPLICANT: Potempa, Jan S.

APPLICANT: Barr, Philip J.

APPLICANT: Pavloff, Nadine

APPLICANT: Pike, Robert N.

TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis

TITLE OF INVENTION: Protease

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Greenlee and Winner, P.C.

STREET: 5370 Manhattan Circle, Suite 201

CITY: Boulder

STATE: CO

COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/541,902

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/141,324

FILING DATE: 21-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 44-93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-541-902-11

Query Match 100.0%; Score 54; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
Db 6 VKMDAEFRHD 15

RESULT 5
US-08-462-859A-5
Sequence 5, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5652092e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-5

Query Match 100.0%; Score 54; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.00033;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VKMDAEFRHD 10
Db 7 VKMDAEFRHD 16

RESULT 6
US-08-123-659A-5
Sequence 5, Application US/08123659A
Patent No. 5656477
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5656477e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-5

Query Match 100.0%; Score 54; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
Db 7 VKMDAEFRHD 16
RESULT 7
US-08-464-247A-5
Sequence 5, Application US/08464247A
Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany

STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/464,247A
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-5

Query Match 100.0%; Score 54; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
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DB 7 VKMDAEFRHD 16

RESULT 8
US-08-464-248A-5
Sequence 5, Application US/08464248A
Patent No. 5703209
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5703209e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-5

Query Match 100.0%; Score 54; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
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DB 7 VKMDAEFRHD 16

RESULT 9
US-09-173-887-5
Sequence 5, Application US/09173887
Patent No. 6245884
GENERAL INFORMATION:
APPLICANT: Hook, Vivian Y.H.
TITLE OF INVENTION: SECRETASES RELATED TO ALZHEIMER'S DEMENTIA
FILE REFERENCE: P-AS 3337
CURRENT APPLICATION NUMBER: US/09/173,887
CURRENT FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 53
TYPE: PRT
ORGANISM: mammalian
US-09-173-887-5

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Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
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DB 1 VKMDAEFRHD 10

RESULT 10
US-08-371-930-25
Sequence 25, Application US/08371930
Patent No. 5578451
GENERAL INFORMATION:
APPLICANT: Nishimoto, Ikuro
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,930
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/019,208
FILING DATE: February 18, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/154001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 58
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-371-930-25

Query Match 100.0%; Score 54; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
DB 44 VKMDAEFRHD 53

RESULT 11
PCT-US94-01712-25
Sequence 25, Application PC/TUS9401712
GENERAL INFORMATION:
APPLICANT: Nishimoto, Ikuro
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/019,208
FILING DATE: February 18, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/154001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 58
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US94-01712-25

Query Match 100.0%; Score 54; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
DB 44 VKMDAEFRHD 53

RESULT 12
US-08-484-969-3
Sequence 3, Application US/08484969
Patent No. 5679531
GENERAL INFORMATION:
APPLICANT: Konig, Gerhard
APPLICANT: Graham, Paul
TITLE OF INVENTION: Monoclonal Antibody Specific for BA4
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allgeiretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,969
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 95,216
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 4..5
OTHER INFORMATION: /label= Beta
OTHER INFORMATION: /note= "Beta cleavage site in App"
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 20..21
OTHER INFORMATION: /label= Alpha
OTHER INFORMATION: /note= "Alpha cleavage site in App, residues 16/17
FEATURE:
NAME/KEY: Cleavage-site
LOCATION: 46..47
OTHER INFORMATION: /label= Gamma
OTHER INFORMATION: /note= "Gamma cleavage site in App"
FEATURE:
NAME/KEY: Peptide
LOCATION: 5..47
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OTHER INFORMATION: /note= "BA4 peptide"
FEATURE:
NAME/KEY: Region
LOCATION: 33..56
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FEATURE:
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LOCATION: 1..32
OTHER INFORMATION: /label= Ex
OTHER INFORMATION: /note= "N-terminal extracellular part of App"
US-08-484-969-3

Query Match 100.0%; Score 54; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VKMDAEFRHD 10
Db 2 VKMDAEFRHD 11

RESULT 13
US-08-472-627-3

; Sequence 3, Application US/08472627
; Patent No. 5693753
; GENERAL INFORMATION:
; APPLICANT: Konig, Gerhard
; APPLICANT: Graham, Paul
; TITLE OF INVENTION: Monoclonal Antibody Specific for BA4
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegratti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,627
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 95,216
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Cleavage-site
; LOCATION: 4.5
; OTHER INFORMATION: /label= Beta
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; US-08-472-627-3

Query Match 100.0%; Score 54; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VKMDAEFRHD 10
Db 2 VKMDAEFRHD 11

RESULT 14

US-08-388-463-3
; Sequence 3, Application US/08388463
; Patent No. 5786180
; GENERAL INFORMATION:
; APPLICANT: Konig, Gerhard
; APPLICANT: Graham, Paul
; TITLE OF INVENTION: Monoclonal Antibody Specific for BA4
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegratti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,463
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 95,216
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Cleavage-site
; LOCATION: 4..5
; OTHER INFORMATION: /label= Beta
; OTHER INFORMATION: /note= "Beta cleavage site in App"
; FEATURE:
; NAME/KEY: Cleavage-site
; LOCATION: 20..21
; OTHER INFORMATION: /label= Alpha
; OTHER INFORMATION: /note= "Alpha cleavage site in App, residues 16/17
; FEATURE:
; NAME/KEY: Cleavage-site
; LOCATION: 46..47
; OTHER INFORMATION: /label= Gamma

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; OTHER INFORMATION: /note= "Gamma cleavage site in App"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 5..47
; OTHER INFORMATION: /label= BA4
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; FEATURE:
; NAME/KEY: Region
; LOCATION: 33..56
; OTHER INFORMATION: /label= Tm
; OTHER INFORMATION: /note= "Transmembrane region of App"
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; LOCATION: 1..32
; OTHER INFORMATION: /label= Ex
; OTHER INFORMATION: /note= "N-terminal extracellular part of App"
; US-08-388-463-3

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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFRHD 10
Db 2 VKMDAEFRHD 11

RESULT 15
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; Sequence 3, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; TITLE OF INVENTION: No. 5652092e1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
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; US-08-462-859A-3

Query Match
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VKMDAEFRHD 10
Db 7 VKMDAEFRHD 16
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Search completed: October 29, 2002, 10:32:08
Job time : 10 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

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(without alignments)
47.995 Million cell updates/sec

Title: US-09-580-018-7
Perfect score: 54
Sequence: 1 KMDAEPFRHDS 10

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
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2	54	100.0	16	21	AA806315
3	54	100.0	16	21	AA806317
4	54	100.0	18	16	AA875696
5	54	100.0	18	22	AA800608
6	54	100.0	19	12	AA814135
7	54	100.0	20	21	AA859713
8	54	100.0	33	20	AA898002
9	54	100.0	39	21	AA869717
10	54	100.0	45	18	AA826512
11	54	100.0	45	18	AA826392

12	54	100.0	45	19	AA844748
13	54	100.0	45	19	AA842977
14	54	100.0	48	22	AA837523
15	54	100.0	50	22	AA865957
16	54	100.0	53	15	AA853695
17	54	100.0	53	15	AA855696
18	54	100.0	53	15	AA855697
19	54	100.0	53	16	AA864168
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22	54	100.0	58	15	AA858937
23	54	100.0	59	17	AA805375
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26	54	100.0	60	21	AA869701
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38	54	100.0	103	19	AA851317
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41	54	100.0	103	21	AA812509
42	54	100.0	104	19	AA851100
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45	54	100.0	117	19	AA851102

ALIGNMENTS

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XX					
AC	AA846211;				
XX					
DT	04-APR-2001	(first entry)			
XX					
DE	Human APP derived immunogenic peptide #7.				
XX					
KW	Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;				
KW	Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;				
KW	amyloid precursor protein; Alzheimer's disease.				
XX					
OS	Homo sapiens.				
XX					
PN	W0200072880-A2.				
XX					
PD	07-DEC-2000.				
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PF	26-MAY-2000; 2000MO-US14810.				
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PR	28-MAY-1999; 99US-0322289.				
XX					
PA	(NEUR-) NEURALAB LTD.				
XX					
PI	Schenk DB, Bard F, Vasquez NJ, Yednock T;				
XX					
DR	WPI; 2001-032104/04.				
XX					
PT	Preventing or treating a disease associated with amyloid deposits,				
PT	especially Alzheimer's disease, comprises administering amyloid				
PT	specific antibody				
XX					

PS Disclosure; Figure 19; 143pp; English.

CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have neurotropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease.

XX Sequence 10 AA:

SO

Query Match 100.0%; Score 54; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAERRHDS 10
DB 1 KMDAERRHDS 10

RESULT 2
AAB06315
ID AAB06315 standard; peptide; 16 AA.

XX AAB06315;
XX
XX
DT 03-OCT-2000 (first entry)
XX
XX Human beta-amyloid precursor protein beta-secretase cleavage site.
XX
XX Human; beta-amyloid precursor protein; beta-APP; beta-secretase;
XX Subtilisin-kexin isoenzyme 1; SKI-1;
XX pro-brain-derived neurotrophic factor; PROBDNF; antilipaeamic;
XX cytostatic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia;
XX liver steatosis; Ras-dependent cancer; restenosis;
XX amyloid protein formation.

XX Homo sapiens.

XX
XX
FH Key Location/Qualifiers
FT Cleavage-site 8..9
XX
XX WO200026348-A2.
XX
XX 11-MAY-2000.
XX
XX 04-NOV-1999; 99WO-CA01058.
XX
XX 04-NOV-1998; 98CA-2249648.
XX
XX (RECL-) INST RECH CLINIQUES MONTREAL.
XX
XX Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;
XX
XX WPI: 2000-365601/31.
XX
XX Novel soluble proteic fragment of subtilisin-kexin isoenzyme for
XX producing a polypeptide useful for treating hypercholesterolemia, liver
XX steatosis and amyloidosis, comprises a specific amino acid sequence -
XX
XX Example 4: Page 51; 119pp; English.
XX
XX The present sequence is the beta-secretase site of human beta-amyloid
XX precursor protein (beta-APP). The sequence may be cleaved
XX by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1
XX (SKI-1), a type-1 membrane-bound proteinase. Peptides which bind to and
XX fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,
XX Ras-dependent cancer, restenosis and amyloid protein formation.

CC are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for
CC screening inhibitors of SKI-1 activity, or for screening enhancers of
CC SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1
CC catalytic site may be used as inhibitors of SKI-1 activity. They may be
CC used to treat diseases involving overexpression of SKI-1 or SKI-1
CC substrate. Such diseases include hypercholesterolaemia, high levels of
CC fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,
CC Ras-dependent cancer, restenosis and amyloid protein formation.

XX Sequence 16 AA:

SO

Query Match 100.0%; Score 54; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAERRHDS 10
DB 7 KMDAERRHDS 16

RESULT 3
AAB06317
ID AAB06317 standard; peptide; 16 AA.

XX AAB06317;
XX
XX
DT 03-OCT-2000 (first entry)
XX
XX Human beta-amyloid precursor protein beta-epsilont-secretase site.
XX
XX Human; beta-amyloid precursor protein; beta-APP;
XX beta-epsilont-secretase; subtilisin-kexin isoenzyme 1; SKI-1;
XX pro-brain-derived neurotrophic factor; PROBDNF; antilipaeamic;
XX cytostatic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia;
XX liver steatosis; Ras-dependent cancer; restenosis;
XX amyloid protein formation.

XX Homo sapiens.

XX
XX
FH Key Location/Qualifiers
FT Cleavage-site 8..9
XX
XX WO200026348-A2.
XX
XX 11-MAY-2000.
XX
XX 04-NOV-1999; 99WO-CA01058.
XX
XX 04-NOV-1998; 98CA-2249648.
XX
XX (RECL-) INST RECH CLINIQUES MONTREAL.
XX
XX Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;
XX
XX WPI: 2000-365601/31.
XX
XX Novel soluble proteic fragment of subtilisin-kexin isoenzyme for
XX producing a polypeptide useful for treating hypercholesterolemia, liver
XX steatosis and amyloidosis, comprises a specific amino acid sequence -
XX
XX Example 4: Page 51; 119pp; English.
XX
XX The present sequence is the beta-epsilont-secretase site of human
XX beta-amyloid precursor protein (beta-APP). The sequence may be cleaved
XX by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1
XX (SKI-1), a type-1 membrane-bound proteinase. Peptides which bind to and
XX are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for
XX screening inhibitors of SKI-1 activity, or for screening enhancers of
XX SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1
XX catalytic site may be used as inhibitors of SKI-1 activity. They may be
XX used to treat diseases involving overexpression of SKI-1 or SKI-1
XX substrate. Such diseases include hypercholesterolaemia, high levels of
XX fatty acids, lipids or farnesyl pyrophosphate, liver steatosis,

CC Ras-dependent cancer, restenosis and amyloid protein formation.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 54; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
| | | | | | | | | |
Db 5 KMDAEFRHDS 14

RESULT 4
AAR75696
ID AAR75696 standard; peptide: 18 AA.
XX
AC AAR75696;

DT 21-JAN-1996 (first entry)
XX

DE Unspecified peptide.
XX

KM Amyloid precursor protein; APP; annexin-V; Alzheimer's disease;
KW disease diagnosis; therapy; antibody.
XX

OS Synthetic.
XX

PN EP655626-A1.
XX

PD 31-MAY-1995.
XX

PF 10-NOV-1994; 94EP-0308309.
XX

PR 10-NOV-1993; 93US-0149975.
XX

PA (MCLE-) MCLEAN HOSPITAL CORP.
XX

PI Honda T, Nixon R;
XX

DR WPI; 1995-195688/26.
XX

PT New peptide(s) associated with Alzheimer's disease - namely p33 and
the amyloid precursor C2 fragment, useful for the prodn. of
diagnostic antibodies
XX

PS Disclosure: Page 13; 32pp; English.
XX

CC Unspecified peptide.
XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 54; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
| | | | | | | | | |
Db 2 KMDAEFRHDS 11

RESULT 5
AAE00608
ID AAE00608 standard; peptide: 18 AA.
XX
AC AAE00608;

DT 02-JUL-2001 (first entry)
XX

DE Beta-amyloid precursor protein beta-secretase cleavage site.
XX

KW Beta-amyloid precursor protein; beta-APP; caspase; beta-secretase;
cysteine protease; apoptosis; caspase expression cassette; metastasis;
XX

KW tumour; cathepsin B; urokinase; proliferation; gene therapy;
KW interdomain linker; cleavage site; Alzheimer's disease.
XX
OS Unidentified.
XX

PN WO200129232-A2.
XX

PD 26-APR-2001.
XX

PF 19-OCT-2000; 2000MO-US28941.
XX

PR 20-OCT-1999; 99US-0160559.
XX

PR 14-AUG-2000; 2000US-0225564.
XX

PA (SCIO-) SCIOS INC.
XX

PI Cordell B, Li Y;
XX

DR WPI; 2001-290920/30.
XX

PT Novel fusion polypeptide comprising first and second caspase subunit
separated by cleavage site not associated in nature with caspase
subunit, useful for cloning gene encoding enzymes involved in
proteolytic cleavage -
XX

PT proteolytic cleavage -
XX

PS Example 2; Page 26; 116pp; English.
XX

CC The present sequence is a beta-secretase cleavage site of beta-amyloid
precursor protein (beta-APP). This sequence is used to construct
an artificially engineered chimeric cassette comprising human caspase-3
with interdomain linker replaced by swedish mutant beta-secretase
cleavage site. This modified caspase-3 plays a pivotal role in
Alzheimer's disease. Caspases are a family of cysteine proteases, that
participate in the initiation and execution of apoptosis.
XX

CC The present invention relates to a method for functional cloning of genes
encoding proteins or enzymes involved in proteolytic cleavage. The
invention is based on the use of caspase expression cassettes comprising
the coding sequence of a proteolytic cleavage site flanked by sequences
encoding two caspase subunits. A fusion polypeptide comprising a first
caspase and a second caspase subunit, separated by a cleavage site not associated
in nature, is useful for cloning gene encoding enzymes involved in
proteolytic cleavage. An expression cassette containing fusion
polypeptide is used to identify a mutant cell line deficient in an
enzyme of interest and is also useful for diagnosis and suppression of
proliferation or metastases of a tumour cell characterised by
overexpression of a polypeptide (e.g. Cathepsin B or urokinase,
selectively expressed in the tumour cells). DNA encoding fusion
polypeptide is used in gene therapy.
XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 54; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
| | | | | | | | | |
Db 9 KMDAEFRHDS 18

RESULT 6
AAR14135
ID AAR14135 standard; peptide: 19 AA.
XX
AC AAR14135;

DT 12-DEC-1991 (first entry)
XX

DE Brain-derived protease substrate contg. beta-APP cleavage site.
XX

KW Alzheimer's disease; chymase; multicatalytic protease;
beta-amyloid precursor protein; A4.
XX

OS Synthetic.
XX
FH Key Location/Qualifiers
FT Cleavage-site 4.5 /note= "chymase and multicatalytic protease site"
XX
XX WO9113904-A.
XX
XX 19-SEP-1991.
XX
XX 04-MAR-1991; 91WO-US01474.
XX
XX 05-MAR-1990; 90US-0489290.
XX
XX (CEPH-) CEPHALON INC.
XX
XX Siman R, Nelson RB, Kauer J, Potter H;
XX WPI; 1991-295576/40.
XX
XX New chymotrypsin-like serine protease(s) - and their inhibitors
PT are used to treat Alzheimer's disease
XX
XX Claim 41; Page 63; 86pp; English.
XX
XX This peptide is designed based on the sequence of beta-APP A4
CC cleavage site. Cleavage by proteases in the brain releases beta-
CC amyloid protein, the deposition of which is a feature of Alzheimer's
CC disease neuropathology. The peptide is used to screen for candidate
CC proteases which cleave between the Met and Asp residues. Two new
CC proteases have been isolated having this cleavage specificity.
CC Chymase was isolated from rat brains and multicatalytic protease was
CC isolated from human cerebral cortex. See also AAR14136-9.
XX
SQ Sequence 19 AA;

Query Match 100.0%; Score 54; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0006;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10
DB 3 KMDAEFRHDS 12

RESULT 7
AAV69713
ID AAV69713 standard; peptide: 20 AA.
XX
XX AAV69713;
XX
XX 11-APR-2000 (first entry)
XX
XX Beta-APP alpha-secretase substrate [KM]-APP(-10,+10).
DE
XX Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
KM cleavage site; beta-secretase; neurodegenerative disease;
KM Alzheimer's disease.
XX
XX Homo sapiens.
OS
XX
XX MO9964587-A1.
XX
XX 16-DEC-1999.
XX
XX 04-JUN-1999; 99WO-FR01326.
XX
XX 05-JUN-1998; 98FR-0007068.
XX
XX 31-MAR-1999; 99US-0122599.
XX
XX (RHON) RHONE-POULENC RORER SA.
PA (UYPA-) UNIV CURIE PARIS VI P 6 M.
XX

PI Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
XX
XX WPI; 2000-097537/08.
XX
XX Polypeptide with beta-secretase activity, specific for wild-type
PT amyloid precursor protein, useful in treating Alzheimer's disease -
XX
XX Example 3; Page 24; 44pp; French.
XX
XX Peptides AAV69702-169718 represent synthetic peptide substrates for a
CC novel polypeptide with beta-secretase activity that can cleave
CC specifically the natural beta-amyloid precursor protein (BAPP). Normal
CC cleavage of the protein occurs between amino acids Met596-Asp597 and
CC Val636-Ile637 (positions 4-5 and 44-45 of AAV69701). The novel
CC polypeptide is used to identify agents that interact specifically with
CC it. These agents regulate metabolism of APP, particularly they slow down
CC or reduce production of beta-amyloid, so can be used to treat
CC neurodegenerative diseases, particularly Alzheimer's disease.
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 54; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10
DB 9 KMDAEFRHDS 18

RESULT 8
AAW98002
ID AAW98002 standard; Protein; 33 AA.
XX
XX AAW98002;
XX
XX 21-JUN-1999 (first entry)
XX
XX Amyloid precursor protein (aa656-678) with Swedish mutation.
DE
XX Amyloid precursor protein; APP; human; gene targeting;
KM homologous recombination; transgenic mouse; transgenic animal;
KW animal model; Alzheimer's disease.
XX
XX Mus musculus.
OS
XX
XX WO9909150-A1.
XX
XX 25-FEB-1999.
XX
XX 18-AUG-1997; 97WO-US14507.
XX
XX 18-AUG-1997; 97WO-US14507.
XX
XX (FARB) BAYER CORP.
PA
XX
XX Wlrak DO;
PI
XX
XX WPI; 1999-181029/15.
XX
XX Modification of target nucleic acids - by homologous recombination,
PT used particularly for introducing a humanised amyloid precursor
PT protein gene into rodents for producing models of Alzheimer's
PT disease
XX
XX disclosure; Page 145; 209pp; English.
XX
XX This polypeptide comprises residues 656-678 of a murine amyloid
CC precursor protein (APP). The invention provides a novel gene
CC targeting strategy that facilitates the introduction of one or
CC more specific mutations into any gene in a single double reciprocal
CC homologous recombination step. The method has been used
CC particularly for introducing a humanised APP gene into rodents for

CC Producing animal models of Alzheimer's disease (AD). 4 Independent
 CC lines of transgenic mice (lines ES5007, ES5103, ES5401 and ES5403)
 CC have been created using the gene targeting technique applied to
 CC embryonic stem cells. In each line, the mouse APP gene was modified
 CC to encode a mouse/human hybrid (m/hAPP) where amino acid residues
 CC 666-770 of APP770 were encoded by human cDNA sequences instead of
 CC mouse genomic exons (exons 16-18). Within these residues, only 3
 CC amino acid differences exist between the mouse and human proteins,
 CC i.e. Gly-676 to Arg, Phe-681 to Thr and Arg-684 to His. The
 CC exon-cDNA fusion gene therefore encodes an APP containing a
 CC humanised beta-amyloid domain. Swedish- and/or London-PAD APP
 CC mutations have also been introduced (see also AAW97997-W98001).

CC Sequence 33 AA;

Query Match 100.0%; Score 54; DB 20; Length 33;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10
 |||||
 DB 15 KMDAEPFRHDS 24

RESULT 9

AA69717
 ID AAY69717 standard; peptide; 39 AA.

AC AAY69717;

DT 11-APR-2000 (first entry)

DE Beta-APP alpha-secretase substrate [KM]-APP(-20,+20).

KM Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
 KM cleavage site; beta-secretase; neurodegenerative disease;

KW Alzheimer's disease.

XX Homo sapiens.

XX WO964587-A1.

PD 16-DEC-1999.

PF 04-JUN-1999; 99WO-FR01326.

PR 05-JUN-1998; 98FR-0007068.

PR 31-MAR-1999; 99US-0122599.

PA (RHON) RHONE-POULENC RORER SA.

PA (UYPA-) UNIV CURIE PARIS VI P & M.

PI Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;

DR WPI; 2000-097537/08.

PT Polypeptide with beta-secretase activity, specific for wild-type
 PT amyloid precursor protein, useful in treating Alzheimer's disease -

PS Example 3; Page 24; 44pp: French.

XX peptides AAY69702-Y69718 represent synthetic peptide substrates for a
 CC novel polypeptide with beta-secretase activity that can cleave
 CC specifically the natural beta-amyloid precursor protein (BAP). Normal
 CC cleavage of the protein occurs between amino acids Met596-Asp597 and
 CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
 CC polypeptide is used to identify agents that interact specifically with
 CC it. These agents regulate metabolism of APP, particularly they slow down
 CC or reduce production of beta-amyloid, so can be used to treat
 CC neurodegenerative diseases, particularly Alzheimer's disease.

SO Sequence 39 AA;

Query Match 100.0%; Score 54; DB 21; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10
 |||||
 DB 18 KMDAEPFRHDS 27

RESULT 10

AAW26512
 ID AAW26512 standard; Peptide; 45 AA.

AC AAW26512;

DT 06-JAN-1998 (first entry)

DE Amyloid precursor protein fragment APP-REP 751 (BAP del11-28).

KM Amyloid precursor protein; APP; beta-amyloid protein; BAP;
 KM substrate; muten; secretase; Alzheimer's disease; human.

XX Chimeric Homo sapiens.

OS Chimeric synthetic.

XX Key Location/Qualifiers

FT Cleavage-site 7..8 /note="secretase cleavage site"

FT Peptide 10..33 /label=BAP(del11-28)

FT /note="truncated beta-amyloid protein"

FT Domain 20..42 /label= Transmembrane

XX US656477-A.

XX 12-AUG-1997.

XX 01-MAY-1992; 92US-0877675.

XX 20-SEP-1993; 93US-0123659.

XX 01-MAY-1992; 92US-0877675.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobsen JS, Vittek MP;

XX WPI; 1997-414594/38.

PT Nucleic acid encoding amyloid precursor muten(s) - comprising
 PT reporter gene and coding sequence, for identifying compounds which
 PT modify the activity of proteolytic enzymes which cleave APP

PS Disclosure; Fig 5A; 84pp: English.

XX This peptide sequence shows the region of amyloid precursor protein
 CC (APP) that includes a truncated beta-amyloid protein (BAP) lacking
 CC the native secretase cleavage/recognition site. In an attempt to
 CC engineer an APP non-cleavable substrate for secretase, an
 CC APP-reporter (APP-RBP) protein that carries the BAP deletion has
 CC been expressed in recombinant host cells. Deletion of these 18
 CC amino acids, however, still resulted in the secretion of an
 CC N-terminal APP-reporter fragment into the cytoplasm. Non-
 CC cleavable APP substrates can be used to detect other putative
 CC abnormal APP processing events. They can also be used to
 CC investigate cellular post-translational modifications to APP in
 CC order to determine the potential influence on normal secretase and
 CC abnormal BAP 'clipping' activities.

SO Sequence 45 AA;

Query Match 100.0%; Score 54; DB 18; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0015;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10
| | | | | | | | | |
Db 8 KMDAEFRHDS 17

RESULT 11

AAW26392
ID AAW26392 standard; Peptide: 45 AA.

XX AAW26392;

DT 15-DEC-1997 (first entry)

DE Amyloid precursor protein fragment APP-REP 751 (BAP del11-28).

KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;

KM substrate; muten; secretase; Alzheimer's disease; human.

XX Chimeric Homo sapiens;

OS Chimeric synthetic.

XX Key Location/Qualifiers

FT Cleavage-site 7..8 /note= "secretase cleavage site"

FT Peptide 10..33

FT /label= BAP(del11-28)

FT /note= "truncated beta-amyloid protein"

FT Domain 20..42

FT /label= Transmembrane

PN US5652092-A.

PD 29-JUL-1997.

PE 01-MAY-1992; 92US-0877675.

PR 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

PR 05-JUN-1995; 95US-0462859.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobsen JS, Vittek MP;

XX WPI; 1997-392937/36.

XX Screening for compounds which reduce beta-amyloid protein formation

PT - using cells which express a construct encoding a marker and an

PT amyloid precursor muten derived from APP isoforms

PS Disclosure; Fig 5A; 84pp; English.

XX This peptide sequence shows the region of amyloid precursor protein

CC (APP) that includes a truncated beta-amyloid protein (BAP) lacking

CC the native secretase cleavage/recognition site. In an attempt to

CC engineer an APP non-cleavable substrate for secretase, an

CC APP-reporter (APP-REP) protein that carries the BAP deletion has

CC been expressed in recombinant host cells. Deletion of these 18

CC amino acids, however, still resulted in the secretion of an

CC N-terminal APP-reporter fragment into the cytoplasm. Non-

CC cleavable APP substrates can be used to detect other putative

CC abnormal APP processing events. They can also be used to

CC investigate cellular post-translational modifications to APP in

CC order to determine the potential influence on normal secretase and

CC abnormal BAP 'clipping' activities.

XX Sequence 45 AA;

QY 1 KMDAEFRHDS 10
| | | | | | | | | |
Db 8 KMDAEFRHDS 17

RESULT 12

AAW44748
ID AAW44748 standard; Protein: 45 AA.

XX AAW44748;

DT 01-JUN-1998 (first entry)

DE APP-REP 751 [BAP delta(11-28)] peptide.

KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;

KM epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;

KW Alzheimer's disease; cleavage.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Cleavage-site 7..8 /note= "putative secretase cleavage site"

FT Misc-difference 19..20 /note= "residues 11-28 of the wild type BAP sequence

FT are deleted from between these positions"

PN US5693478-A.

PD 02-DEC-1997.

PE 05-JUN-1995; 95US-0464247.

PR 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

PR 05-JUN-1995; 95US-0464247.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobsen JS, Vittek MP;

XX WPI; 1998-031744/03.

XX Amyloid precursor muten reporter molecule assay containing antibody

PT recognised marker - used to study pathways associated with

PT Alzheimer's disease

PS Disclosure; Fig 5A; 84pp; English.

XX This sequence represent the beta-amyloid protein sequence from the

CC construct APP-REP751 [BAP delta(11-28)]. The mutant sequence contains

CC a deletion of the wild type BAP residues 11-28. This causes a

CC shortening of the BAP sequence. This may affect cleavage of the BAP by

CC the "secretase" dependent on whether the "secretase" recognises the

CC cleavage site by a positional effect or by sequence. The mutant sequence

CC can be used in a method to study secretase and beta-amyloid protein

CC (BAP)-generating pathways associated with Alzheimer's disease by

CC studying proteolytic cleavage of the reporter polypeptides (e.g.

CC AAW44744 and AAW44745).

XX Sequence 45 AA;

QY Query Match 100.0%; Score 54; DB 19; Length 45;

Best Local Similarity 100.0%; Pred. No. 0.0015;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10
| | | | | | | | | |
Db 8 KMDAEFRHDS 17

RESULT 13

AA042977 standard; peptide: 45 AA.

AA042977:

01-MAY-1998 (first entry)

Deletion beta-amyloid peptide (BAP) derived from APP-REP 751.

Beta-amyloid peptide; BAP; extracellular BAP plaque;

cerebrovascular deposit; Alzheimer's disease; Downs syndrome;

amyloid precursor protein; APP; secretase; BAP aggregation;

abnormal proteolytic cleavage.

Homo sapiens.

Key Domain

Location/Qualifiers

20..43

/note="putative transmembrane domain"

US5703209-A.

30-DEC-1997.

05-JUN-1995; 95US-0464248.

20-SEP-1993; 93US-0123659.

01-MAY-1992; 92US-0877675.

(AMCY) AMERICAN CYANAMID CO.

Jacobson JS, Vitek MP;

WPI: 1998-076482/07.

Amyloid precursor protein fusion polypeptides - comprising APP

fragment and marker, useful for research and drug screening

Disclosure; Fig 5A: 84pp; English.

The present sequence represents a beta-amyloid peptide (BAP), with

a deletion amino acids 11-28 (numbered according to AA042976). Abnormal

accumulation of extracellular BAP in plaques and cerebrovascular

deposits is characteristic in brains of individuals suffering from

Alzheimer's disease and Downs syndrome. BAP is a poorly soluble,

self-aggregating protein which is derived from a larger amyloid precursor

protein (APP). APP is expressed as an integral membrane protein and is

cleaved by secretase, between BAP 16lys and 17leu. Cleavage at this site

precludes amyloidogenesis and results in the release of the

amino-terminal APP fragment. Three major isoforms of APP exist: APP-695,

APP-751 and APP-770. These isoforms are derived by alternative splicing.

APP-APP 751 is a deletion construct of APP-751, which has a deletion of

2/6 amino acids to within 15 amino acids of the BAP domain. APP can be

used as a substrate for studying abnormal proteolytic cleavage which

results in the release of BAP, and also to screen for drugs that will

inhibit such cleavage.

Sequence 45 AA:

Query Match 100.0%; Score 54; DB 19; Length 45;

Best Local Similarity 100.0%; Pred. No. 0.0015;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KMDAEPFRHDS 10

8 KMDAEPFRHDS 17

RESULT 14

AA037523

AA037523 standard; peptide: 48 AA.

AA037523

AA037523

AA037523;

01-MAR-2001 (first entry)

Amyloid precursor protein APP residues 669-716.

Amyloid precursor protein; APP; Alzheimer's disease; Abeta.

Unidentified.

WO200066181-A1.

09-NOV-2000.

01-MAY-2000; 2000WO-US11715.

29-APR-1999; 99US-0131579.

(GENO) GEN HOSPITAL CORP.

Bush AI, Huang X, Atwood CS, Tanzi RE;

WPI: 2001-015918/02.

Screening for agents useful in treating Alzheimer's disease by adding

the agent to an Abeta-containing sample and detecting inhibition of

oxygen-dependent hydrogen peroxide formation by the agent.

Disclosure; Fig 6; 98pp; English.

The present invention relates to methods for identifying agents which

can be used in the treatment of Alzheimer's disease. These agents are

identified for their ability to inhibit oxygen-dependent hydrogen

peroxide formation but their inability to inhibit superoxide-dependent

hydrogen peroxide formation. This means that they decrease the

neurotoxicity of Abeta, the protein which is thought to cause Alzheimer's

disease.

Sequence 48 AA:

Query Match 100.0%; Score 54; DB 22; Length 48;

Best Local Similarity 100.0%; Pred. No. 0.0016;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KMDAEPFRHDS 10

2 KMDAEPFRHDS 11

RESULT 15

AA065957

AA065957 standard; protein: 50 AA.

AA065957;

11-FEB-2002 (first entry)

Human A4 amyloid precursor protein partial sequence.

Alpha 7 nicotinic receptor; acetylcholinesterase; AChE; synaptica;

antiparkinsonian; nootropic; neuroprotective; Alzheimer's disease;

motor neuron disease; A4 amyloid precursor protein.

Homo sapiens.

WO200173446-A1.

04-OCT-2001.

29-MAR-2001; 2001WO-GB01401.

29-MAR-2000; 2000GB-0007630.

PR 15-DEC-2000; 2000GB-0030660.

XX
PA (SYNA-) SYNAPTICA LTD.
PA (GREN/) GREENFIELD S A.
XX
XX
PI Westwell M;
XX
DR WPI; 2001-639255/73.

XX
XX
PR Use of alpha 7 nicotinic receptor or its functional analog to determine
PR if a compound is capable of acting as functional analog or antagonist
PR of acetylcholinesterase polypeptide for treating neurological disorders
PR
XX
XX

PS Disclosure; Fig 1; 45pp; English.

XX
XX
CC The invention relates to the use of an alpha 7 nicotinic receptor (I) or
CC its functional analog to determine whether a compound is capable of
CC acting as a functional analog or antagonist of an acetylcholinesterase
CC (AChE) polypeptide fragment (Synaptica peptide) on (I). If (I) is a
CC native alpha 7 nicotinic receptor in its normal membrane environment, it
CC is identified by means of inhibition by a blocker of (I). Methods for
CC identifying a functional analog or antagonist of the synaptica peptide
CC are also provided. The identified functional analog or antagonist is
CC useful for the preparation of a medicament for treatment of a
CC neurological disorder associated with non-enzymatic action of AChE, where
CC the neurological disorder is Alzheimer's disease, Parkinson's disease or
CC motor neuron disease. It is useful for inhibiting or preventing non-
CC enzymatic activity of the synaptica peptide in vivo. The present sequence
CC represents a human A4 amyloid precursor protein partial sequence.
XX

SO Sequence 50 AA;

Query Match 100.0%; Score 54; DB 22; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
|||||||
Db 15 KMDAEFRHDS 24

Search completed: October 29, 2002, 10:26:45
Job time : 24.1429 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:36 ; Search time 10.4286 Seconds
(Without alignments)
92.140 Million cell updates/sec

Title: US-09-580-018-7
Perfect score: 54
Sequence: 1 KMDAEFRHDS 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	57	2 E60045	Alzheimer's disease
2	54	100.0	57	2 E60045	Alzheimer's disease
3	54	100.0	57	2 G60045	Alzheimer's disease
4	54	100.0	57	2 D60045	Alzheimer's disease
5	54	100.0	57	2 A60045	Alzheimer's disease
6	54	100.0	57	2 B60045	Alzheimer's disease
7	54	100.0	82	2 P00438	Alzheimer's disease
8	54	100.0	695	1 A49795	Alzheimer's disease
9	54	100.0	770	1 GRH04	Alzheimer's disease
10	47	87.0	33	2 S23094	beta-amyloid prote
11	47	87.0	695	2 A27485	Alzheimer's disease
12	47	87.0	695	2 S00550	Alzheimer's disease
13	45	83.3	747	2 JH0773	Alzheimer's disease
14	44	81.5	42	2 PN0512	beta-amyloid prote
15	39	72.2	511	2 A56750	archain - human
16	35	64.8	428	2 T84320	probable two-compo
17	35	64.8	543	2 T88239	hypothetical prote
18	35	64.8	802	2 A83125	probable TonB-depe
19	35	64.8	900	2 E83189	protein-PII uridy
20	34	63.0	213	2 F87699	conserved hypothet
21	34	63.0	246	2 AG1140	transcription regu
22	34	63.0	400	2 S70187	44.7K vira protein
23	34	63.0	901	2 G89810	conserved hypothet
24	34	63.0	478	2 C70179	probable glycosyl
25	34	63.0	1237	2 A21915	hypothetical prote
26	34	63.0	1256	2 AB2042	hypothetical prote
27	33	61.1	128	2 S69856	hypothetical prote
28	33	61.1	142	2 E89026	protein F13A2.1 [1
29	33	61.1	316	2 T46000	hypothetical prote

30	33	61.1	322	2 A69963	hypothetical prote
31	33	61.1	336	2 AF2085	transcription regu
32	33	61.1	344	2 T23374	hypothetical prote
33	33	61.1	376	2 B84277	hypothetical prote
34	33	61.1	578	2 DB2053	fibriol assembly
35	33	61.1	647	2 T26240	hypothetical prote
36	33	61.1	849	2 T01286	probable RNA-bind
37	33	61.1	927	2 T38127	phosphoprotein - f
38	33	61.1	931	2 A49737	diacylglycerol aminope
39	33	61.1	1524	2 S68553	surface layer prot
40	32	59.3	55	2 C82565	hypothetical prote
41	32	59.3	113	2 AH0923	conserved hypothet
42	32	59.3	160	2 A11308	dihydrofolate redu
43	32	59.3	161	2 S30698	cyax protein - Esc
44	32	59.3	193	2 I50693	interferon - chick
45	32	59.3	213	2 A46237	actin-myosin netwo

ALIGNMENTS

RESULT 1

E60045 Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C:Species: Ovis sp. (sheep)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: E60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <10H>
A:Cross-References: EMBL:X56130
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 54; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10
Db 4 KMDAEFRHDS 13

RESULT 2

F60045 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: F60045
A:Molecule type: mRNA
A:Residues: 1-57 <10H>
A:Cross-References: EMBL:X56127; NID:q1895; PIDN:CAA39592.1; PID:q1896
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 54; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10
Db 4 KMDAEFRHDS 13

RESULT 3
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 54; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10
Db 4 KMDAEPFRHDS 13

RESULT 4
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: D60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56124
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 54; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10
Db 4 KMDAEPFRHDS 13

RESULT 5
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 54; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10
Db 4 KMDAEPFRHDS 13

RESULT 6
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56128; NID:92165; PIDN:CAA39593.1; PID:92166
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 54; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10
Db 4 KMDAEPFRHDS 13

RESULT 7
P00438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: P00438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Marcun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
A:Reference number: P00438; MUID:93075180
A:Accession: P00438
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:M83558; GB:M83657
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 54; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEPFRHDS 10
Db 15 KMDAEPFRHDS 24

RESULT 8
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991

A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a
 A:Reference number: A49795; MUID:91273117
 A:Accession: A49795
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-695 <POD>
 A:Cross-references: GB:M58727; NID:q342062; PIDN:AAA36829.1; PID:q342063
 A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C:Keywords: alternative splicing

Query Match 100.0%; Score 54; DB 1; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.008;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAERRHDS 10
 |||||
 Db 595 KMDAERRHDS 604

RESULT 9
 ORHUA4
 Alzheimer's disease amyloid beta protein precursor [validated] - human
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibi
 N:Contents: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
 protein precursor splice form APP(770)
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-1987 #sequence revision 28-Jul-1995 #text change 15-Sep-2000
 C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I59562; A44
 4668; A28683; A29302; A60805; J10036; S06121; A60355; A59011; A33844; S29076; S38252; S3
 Nucleic Acid Res. 17, 517-522, 1989
 A:Title: The PRA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
 A:Reference number: S02260; MUID:89128427
 A:Accession: S02260
 A:Molecule type: DNA
 A:Residues: 1-288, 'V', 365-770 <LEM1>
 A:Cross-references: EMBL:X13466
 A:Note: alternative splice form APP(695)
 R:Lemaire, H.G.
 submitted to the EMBL Data Library, November 1988
 A:Reference number: S05194
 A:Accession: S05194
 A:Molecule type: DNA
 A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
 A:Cross-references: EMBL:X13466; NID:q35598; PIDN:CAA31830.1; PID:g871360
 A:Note: alternative splice form APP(695)
 R:Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote
 A:Reference number: A32277; MUID:89165870
 A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <LAF>
 A:Cross-references: GB:M24546; GB:M24547; NID:q341202; PIDN:AAIC3654.1; PID:g516074
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
 A:Reference number: A33260; MUID:89392030
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 656-737 <JOH>
 A:Cross-references: GB:M29270; NID:q178863; PIDN:AA51768.1; PID:g178865
 R:Prelli, F.; Levy, E.; Van Duijn, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
 A:Reference number: A35486; MUID:90321244
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRE1>
 A:Note: 693-Gln was found in DNA isolated from HCHMA-D patients
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 87, 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.

A:Reference number: I39451; MUID:90236318
 A:Accession: I39452
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: GB:M33112; NID:q178613; PIDN:AA59502.1; PID:q178616
 A:Accession: I39451
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/
 A:Molecule type: DNA
 A:Residues: 1-530, 'QWLMPIVPAFWKAKGR' <YOS2>
 A:Cross-references: GB:M34875; NID:q178608; PIDN:AA59501.1; PID:q178615
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168
 A:Contents: annotation; erratum
 A:Note: revised physical map for reference I39451
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du
 Science 248, 1124-1126, 1990
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo
 A:Reference number: I39453; MUID:90260663
 A:Accession: I39453
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: GB:M37896; NID:q178618; PIDN:AA51727.1; PID:q178620
 A:Note: a mutation with 693-Gln is presented
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe
 A:Reference number: I59562; MUID:92022553
 A:Accession: I59562
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716, 'F', 718-737 <MUR>
 A:Cross-references: GB:S57665; NID:q236720; PIDN:AA61991.1; PID:q236721
 R:Kamino, K.; Orr, H.T.; Payami, H.; Wilsman, E.M.; Alonso, M.E.; Puls, S.M.; Anders
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Mart
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t
 A:Reference number: A44017; MUID:93053597
 A:Accession: A44017
 A:Molecule type: DNA
 A:Residues: 687-692, 'G', 694-718 <KAM1>
 A:Cross-references: GB:S45135; NID:q257377; PIDN:AA62646.1; PID:q257378
 A:Experimental source: familial Alzheimer disease family SB
 A:Note: sequence extracted from NCBI backbone (NCBI:115374)
 A:Accession: B44017
 A:Molecule type: DNA
 A:Residues: 687-718 <KAM2>
 A:Cross-references: GB:S45136; NID:q257379; PIDN:AA62646.1; PID:q257380
 A:Experimental source: familial Alzheimer disease family LIT
 A:Note: sequence extracted from NCBI backbone (NCBI:115376)
 R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.
 Nature 325, 733-736, 1987
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-sur
 A:Reference number: A03134; MUID:87144572
 A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288, 'V', 365-770 <KAN>
 A:Cross-references: GB:X00264; NID:q28525; PIDN:CAA68374.1; PID:g28526
 A:Note: alternative splice form APP(695)
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascula
 A:Reference number: A29030; MUID:87231971
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A:Cross-references: GB:M16765; NID:q178539; PIDN:AA51722.1; PID:q178540
 A:Note: the authors translated the codon GAG for residue 647 as Asp
 R:Goldberger, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987

A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
 A:Reference number: A47584; MUID:87120328
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756, 'S', 758-770 <GOL>
 A:Cross-references: GB:M15533; NID:9178705; PIDN:AAA5540.1; PID:9178707
 A:Experimental source: brain
 R:Tanai, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
 Science 235, 880-884, 1987
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
 A:Reference number: A47585; MUID:87120329
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TAN1>
 A:Cross-references: GB:M15532; NID:9177957; PIDN:AAA51564.1; PID:9177958
 R:Dykes, T.; Weidmann, A.; Mulhapp, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
 EMBO J. 7, 949-957, 1988
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
 A:Reference number: S02638; MUID:88296437
 A:Accession: S02638
 A:Molecule type: mRNA
 A:Residues: 672-678 <DYR>
 R:Tanai, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
 Nature 331, 528-530, 1988
 A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
 A:Reference number: S00707; MUID:88122640
 A:Accession: S00707
 A:Molecule type: mRNA
 A:Residues: 286-344, 'I', 365-366 <TAN2>
 A:Cross-references: EMBL:X06982; NID:928817; PIDN:CAA30042.1; PID:9292612
 A:Experimental source: promyelocytic leukemia cell line HL60
 A:Note: alternative splice form App(751)
 R:Ponte, P.; Gonzalez-Demitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; De
 Nature 331, 525-527, 1988
 A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
 A:Reference number: S00925; MUID:88122639
 A:Accession: S00925
 A:Molecule type: mRNA
 A:Residues: 1-344, 'I', 365-770 <PO2>
 A:Cross-references: GB:X06989; EMBL:Y00297; NID:928720; PIDN:CAA30050.1; PID:928721
 A:Note: alternative splice form App(775)
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-533, 1988
 A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
 A:Reference number: A38949; MUID:88122641
 A:Accession: A38949
 A:Molecule type: mRNA
 A:Residues: 287-367 <KIT>
 A:Cross-references: GB:X06981; NID:928816; PIDN:CAA30041.1; PID:9292611
 A:Experimental source: glioblastoma cell line
 A:Note: alternative splice form App(770)
 R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three F
 A:Reference number: A30320
 A:Accession: A30320
 A:Molecule type: mRNA
 A:Status: not compared with conceptual translation
 A:Residues: 284-288, 'V', 365-770 <VIT1>
 A:Accession: B30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 122-288, 'V', 365-770 <VIT2>
 A:Accession: C30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 606-770 <VIT3>
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
 A:Reference number: A31087; MUID:88124954
 A:Accession: A31087
 A:Molecule type: mRNA

A:Residues: 507-770 <ZAI>
 A:Cross-references: GB:M18734; NID:9178572; PIDN:AAA51726.1; PID:9178573
 A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue
 8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue
 A:Note: the cited Genbank accession number, J03594, is not in release 101.0
 R:Masters, C.L.; Mulhapp, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther,
 Query Match 100.0%; Score 54; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.0089;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KMDAEFRHDS 10
 |||||
 Db 670 KMDAEFRHDS 679
 RESULT 10
 S23094
 beta-amyloid protein precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
 C:Accession: S23094
 R:Kojima, S.; Omori, M.
 FEBS Lett. 304, 57-60, 1992
 A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic protein
 A:Reference number: S23094; MUID:92316198
 A:Accession: S23094
 A:Molecule type: protein
 A:Residues: 1-33 <KOJ>
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Knitz-type proteinas
 Query Match 87.0%; Score 47; DB 2; Length 33;
 Best Local Similarity 90.0%; Pred. No. 0.0071;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KMDAEFRHDS 10
 |||||
 Db 4 KMDAEFGHDS 13
 RESULT 11
 A27485
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
 N:Alternate names: proteinase nexin II
 C:Species: Mus musculus (house mouse)
 C>Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
 C:Accession: A27485; S19727; I49485
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein pr
 A:Reference number: A27485; MUID:88106489
 A:Accession: A27485
 A:Molecule type: mRNA
 A:Residues: 1-695 <YAM>
 A:Cross-references: GB:M18373; NID:9191568; PIDN:AAA37139.1; PID:9309085
 A:Experimental source: brain
 R:de Strooper, B.; van Leuven, F.; van den Bergh, H.
 Biochim. Biophys. Acta 1129, 141-143, 1991
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is clos
 A:Reference number: S19727; MUID:92096458
 A:Accession: S19727
 A:Molecule type: mRNA
 A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
 A:Cross-references: EMBL:X59379
 R:Itami, R.; Yamada, T.; Yoshikata, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.
 Gene 112, 189-195, 1992
 A:Title: Positive and negative regulatory elements for the expression of the Alzheim
 A:Reference number: I49485; MUID:92209998
 A:Accession: I49485
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-19 <RES>
 A:Cross-references: GB:D10603; NID:9220328; PIDN:BAA01456.1; PID:9220329

C:Genetics:
A:Map position: 16c3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 87.0%; Score 47; DB 2; Length 695;
Best Local Similarity 90.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KMDAERHDS 10
|||||
Db 595 KMDAERGHDS 604

RESULT 12
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C:Accession: S00550; A41245; A39820; S46251
R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A:Reference number: S00550; MUID:88312583
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SHI>
A:Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
R:Schubert, D.; Schroeder, R.; Lacombiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A:Reference number: A41245; MUID:88264430
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A:Note: evidence for heparan sulfate attachment
R:Hesse, L.; Behner, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MUID:94320627
A:Accession: S46251
A:Contents: annotation; copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A:Reference number: A39820; MUID:91217087
A:Accession: A39820
A>Status: preliminary
A:Molecule type: protein
A:Residues: 18-32 <POT>
A:Experimental source: brain
A:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-646/Domain: transmembrane #status Predicted <TM>

Query Match 87.0%; Score 47; DB 2; Length 695;
Best Local Similarity 90.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KMDAERHDS 10
|||||
Db 595 KMDAERGHDS 604

RESULT 13
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773
R:Okado, H.; Okamoto, H.

Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: development
A:Reference number: JH0773; MUID:93129227
A:Accession: JH0773

A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 83.3%; Score 45; DB 2; Length 747;
Best Local Similarity 70.0%; Pred. No. 0.56;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 KMDAERHDS 10
|||||
Db 647 KMDSEYRHDY 656

RESULT 14
PN0512
beta-amyloid protein - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: PN0512
R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragment
A:Reference number: PN0512; MUID:93290653
A:Accession: PN0512
A:Molecule type: protein
A:Residues: 1-42 <SHI>
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid

Query Match 81.5%; Score 44; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 DAERFHDHDS 10
|||||
Db 1 DAERFHDHDS 8

RESULT 15
A56750
archaia - human
C:Species: Homo sapiens (man)
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jul-2000
C:Accession: A56750
R:Radice, P.; Pensotti, V.; Jones, C.; Perry, H.; Pierotti, M.A.; Tunnacliffe, A.
Genomics 26, 101-106, 1995
A:Title: The human archaia gene, ARCN1, has highly conserved homologs in rice and Dro
A:Reference number: A56750; MUID:95301274
A:Accession: A56750
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-511 <RAD>
A:Cross-references: GB:X81197; NID:g773572; PIDN:CAA57071.1; PID:g773573
C:Genetics:
A:Gene: GDB:ARCN1
A:Cross-references: GDB:377806; OMIM:600820
A:Map position: 11q23.3-11q23.3

Query Match 72.2%; Score 39; DB 2; Length 511;
Best Local Similarity 60.0%; Pred. No. 6;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 KMDAERHDS 10
|||||
Db 424 EIDGFRHDS 433

Tue Oct 29 11:23:40 2002

us-09-580-018-7.rpr

Page 6

Search completed: October 29, 2002, 10:31:05
Job time : 11.4286 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:22:36 ; Search time 5 Seconds

(without alignments)
77.439 Million cell updates/sec

Title: US-09-580-018-7

Perfect score: 54

Sequence: 1 KMDAEFRHDS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	57	1 A4_PIG	Q29023 sus scrofa
2	54	100.0	57	1 A4_URSA	Q29149 ursus marit
3	54	100.0	58	1 A4_CANFA	Q28280 canis faml
4	54	100.0	58	1 A4_RABIT	Q28748 oryctolagus
5	54	100.0	58	1 A4_SHEEP	Q28753 ovis aries
6	54	100.0	59	1 A4_BOVIN	Q28053 bos taurus
7	54	100.0	751	1 A4_SAISC	Q95241 salmisi sci
8	54	100.0	770	1 A4_HUMAN	P05067 homo sapien
9	47	87.0	770	1 A4_MOUSE	P12023 mus musculu
10	47	87.0	770	1 A4_RAT	P08592 ratius norv
11	39	72.2	511	1 COPD_BOVIN	P53619 bos taurus
12	39	72.2	511	1 COPD_HUMAN	P48444 homo sapien
13	35	64.8	269	1 T2S1_STRPT	O55152 streptomyce
14	35	64.8	900	1 GLND_PSEBA	Q929H0 pseudomonas
15	34	63.0	478	1 GEPD_BORBU	O51581 borrellia bu
16	33	61.1	322	1 YQVA_BACSV	P54538 bacillus su
17	33	61.1	492	1 C133_DROME	O9yqb3 drosophila
18	33	61.1	500	1 STCL_EMENT	O00707 emeticella
19	33	61.1	927	1 C015_SCHPO	O09822 schizosacch
20	33	61.1	931	1 DAP1_DROME	P33894 saccharomyc
21	32	59.3	107	1 T2AH_DROME	O9w5b9 drosophila
22	32	59.3	161	1 Y2CX_ECOLI	P11291 escherichia
23	32	59.3	193	1 INFL_CHICK	P42165 gallus gall
24	32	59.3	193	1 INFL_CHICK	O90872 gallus gall
25	32	59.3	213	1 NULL_DROME	P33845 drosophila
26	32	59.3	328	1 P2Y3_MEIGA	O93361 meleagris g
27	32	59.3	402	1 RDS1_SCHPO	P53693 schizosacch
28	32	59.3	502	1 YGCL_ECOLI	Q46901 escherichia
29	32	59.3	780	1 TREB_YEAST	P35172 saccharomyc
30	32	59.3	1092	1 DP21_METTH	O27579 methanobact
31	32	59.3	1159	1 DPA3_PASBU	O9cpk3 pasteurella
32	31	58.3	497	1 DHAL_ENCRU	Q27640 encyrtiraeus
33	31	57.4	190	1 GP38_BPSPI	O4394 bacterioph

34	31	57.4	351	1 VA0D_HUMAN	P12953 homo sapien
35	31	57.4	351	1 VA0D_MOUSE	P51863 mus musculu
36	31	57.4	391	1 NCAP_BRSEA	P22677 bovine resp
37	31	57.4	391	1 NCAP_BRSVR	O65708 bovine resp
38	31	57.4	391	1 NCAP_HRSV1	P24566 human resp
39	31	57.4	391	1 NCAP_HRSVA	P03418 human resp
40	31	57.4	391	1 NCAP_ORSVW	O83957 ovine resp
41	31	57.4	413	1 NCAP_ORHCA	O07310 rhodobacter
42	31	57.4	431	1 NCAP_ORHCA	P74384 synecocyst
43	31	57.4	449	1 PURB_SYNY3	O61312 mus musculu
44	31	57.4	453	1 AP2C_MOUSE	P34252 saccharomyc
45	31	57.4	497	1 YK8B_YEAST	O42897 schizosacch

ALIGNMENTS

RESULT 1
A4_PIG STANDARD: PRT: 57 AA.

AC Q29023:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.

OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.

PC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.R., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).

-I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COMPLETS TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
G(O) (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: Type I membrane protein.
-I- SIMILARITY: BELONGS TO THE APP FAMILY.

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CC EMBL: X56127; CAA39592.1; -.
DR HSSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 6 48
FT DOMAIN <1 33
FT TRANSMEM 34 57
FT NON_TER 57
SQ SEQUENCE 57 AA: 6172 MW: 84209088EBA82DFA CRC64;

Query Match 100.0%; Score 54; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KMDAEFRHDS 10
|||||||

Db 4 KMDAERRHDS 13

RESULT 2

A4_URSWA STANDARD; PRT; 57 AA.

AC 029149;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).

GN APP.

OS Ursus maritimus (Polar bear) (Thalartos maritimus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.

OX NCBI_TaxID=29073;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species RT polymerase chain reaction analysis."

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

RL

CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -----

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CC -----

CC EMBL: X56128; CAA39593.1; -.

DR HSSP: P05067; IBA4.

DR InterPro: IPR001868; A4_APP.

DR PROSITE: PS00319; A4_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4_INTRA; PARTIAL.

KM Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER 1 1

FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 34 57 POTENTIAL.

FT NON_TER 57 57

SO SEQUENCE 57 AA; 6172 MW; 84209D88BA82DFA CRC64;

Query Match 100.0%; Score 54; DB 1; Length 57;

Best Local Similarity 100.0%; Pred. No. 0.00024;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KMDAERRHDS 10

Db 4 KMDAERRHDS 13

RESULT 3

A4_CANFA STANDARD; PRT; 58 AA.

AC 028280;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).

GN APP.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species RT polymerase chain reaction analysis."

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

RL

CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -----

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CC -----

CC EMBL: X56125; CAA39590.1; -.

DR HSSP: P05067; IBA4.

DR InterPro: IPR001868; A4_APP.

DR PROSITE: PS00319; A4_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4_INTRA; PARTIAL.

KM Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER 1 1

FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 35 58 POTENTIAL.

FT NON_TER 58 58

SO SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match 100.0%; Score 54; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 0.00024;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KMDAERRHDS 10

Db 5 KMDAERRHDS 14

RESULT 4

A4_RABIT STANDARD; PRT; 58 AA.

AC 028748;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).

GN APP.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species RT polymerase chain reaction analysis."

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

RL

CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

```
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: X56129; CAA39594.1; -.
DR      HSSP: P05067; 1BA4.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1
FT      CHAIN      1
FT      DOMAIN      6 48      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN      <1 33      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      34 57      POTENTIAL.
FT      DOMAIN      58 >58      CYTOPLASMIC (POTENTIAL).
FT      NON_TER      58
SQ      SEQUENCE      58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match      100.0%; Score 54; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 KMDAEFRHDS 10
Db      4 KMDAEFRHDS 13

RESULT 5
A4_SHEEP
ID      A4_SHEEP      STANDARD;      PRT;      58 AA.
AC      Q28757;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-Ap) (A-beta)] (Fragment).
GN      APP.
OS      Ovis aries (Sheep).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Caprinae; Ovis.
OX      NCBI_TaxID=9940;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Heart;
RA      MEDLINE=92017079; PubMed=1656157;
RA      Johnson E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
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DR      EMBL: X56130; CAA39595.1; -.
DR      HSSP: P05067; 1AHL.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1
FT      CHAIN      1
FT      DOMAIN      6 48      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN      <1 33      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      34 57      POTENTIAL.
FT      DOMAIN      58 >58      CYTOPLASMIC (POTENTIAL).
FT      NON_TER      58
SQ      SEQUENCE      58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match      100.0%; Score 54; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 KMDAEFRHDS 10
Db      4 KMDAEFRHDS 13

RESULT 6
A4_BOVIN
ID      A4_BOVIN      STANDARD;      PRT;      59 AA.
AC      Q28053;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-Ap) (A-beta)] (Fragment).
GN      APP.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      MEDLINE=92017079; PubMed=1656157;
RA      Johnson E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: X56124; CAA39589.1; -.
DR      EMBL: X56126; CAA39591.1; -.
DR      HSSP: P05067; 1BA4.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1
FT      CHAIN      1
FT      DOMAIN      7 49      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN      <1 34      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      35 58      POTENTIAL.
FT      DOMAIN      59 >59      CYTOPLASMIC (POTENTIAL).
FT      DOMAIN      59
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FT NON_TER 59 59
SQ SEQUENCE 59 AA: 6414 MW: F43469D48A2E12D CRC64;

Query Match 100.0%; Score 54; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
Db 5 KMDAEFRHDS 14

RESULT 7
A4_SAISC STANDARD; PRT; 751 AA.
AC 095241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
GN APP.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96108492; Pubmed=8532114;
RA Levy E., Amorim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy.";
RL Neurobiol. Aging 16:805-808(1995).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
DR EMBL: S81024; AAD14347.1; -.
DR HSSP: P05067; IAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
KW Signal; Serine protease inhibitor.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 751 A4 PROTEIN.
FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).

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FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 681 704 POTENTIAL.
FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
FT ACT_SITE 301 302 REACTIVE BOND.
FT DISULFID 291 341 BY SIMILARITY.
FT DISULFID 300 324 BY SIMILARITY.
FT DISULFID 316 337 BY SIMILARITY.
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 751 AA: 84893 MW: 6C3E431089569049 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 751;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
Db 651 KMDAEFRHDS 660

RESULT 8
A4_HUMAN STANDARD; PRT; 770 AA.
ID A4_HUMAN
AC P05067; P09000; Q16011;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II) (PN-II) (APPI) [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
GN APP OR A4 OR CVAP OR ADL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain.
RX MEDLINE=87144572; Pubmed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grieschlik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor.";
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88122639; Pubmed=2893289;
RA Ponte P., Gonzalez-Dewhilt P., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors.";
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89128427; Pubmed=2783775;
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97263807; Pubmed=9108164;
RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M., Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for sequencing of a 300 kb region of human APP locus.";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [5]
RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
RX MEDLINE=88122640; Pubmed=2893290;

```

RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
RL Nature 331:528-530(1988).
[6]
RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
[7]
RN SEQUENCE OF 284-289 AND 365-770 FROM N.A.
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
[8]
RN SEQUENCE OF 507-770 FROM N.A.
RP MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
[9]
RN SEQUENCE OF 672-681.
RP MEDLINE=88035004; PubMed=3312495;
RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
RA Tountellotte W.W., Huebner V., Shively J.E.;
RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
RT and partial sequence of a 4,200-dalton peptide isolated from cortical
RT microvessels.";
RL J. Neurochem. 49:1394-1401(1987).
[10]
RN SEQUENCE OF 739-770 FROM N.A.
RP MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";
RL Gene 87:257-263(1990).
[11]
RN SEQUENCE OF 1-10 FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
[12]
RN SEQUENCE OF 18-50.
RP MEDLINE=87250462; PubMed=3597385;
RA Van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
[13]
RN IDENTITY OF APP WITH NEXIN-II.
RX MEDLINE=89384866; PubMed=2506449;
RA Oltersdorf T., Filtz L.C., Schenk D.B., Lieberburg I.,
RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
RA Sinha S.;
RT "The secreted form of the Alzheimer's amyloid precursor protein with
RT the Kunitz domain is protease nexin-II.";
RL Nature 341:144-147(1989).
[14]
RN PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
RX MEDLINE=90211252; PubMed=1969731;
RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
RT disease amyloid protein precursor.";

RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
RN [15]
RP COMPLEX WITH G(O).
RX MEDLINE=93188965; PubMed=8446172;
RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
RA Murayama Y., Ogata E.;
RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
RT protein G(O).";
RL Nature 362:75-79(1993).
[16]
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
RX MEDLINE=99213582; PubMed=10201399;
RA Rossjohn J., Cappai R., Fell S.C., Henry A., Mckinstrey W.J.,
RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
RA Parker M.W.;
RT "Crystal structure of the N-terminal, growth factor-like domain of
RT Alzheimer amyloid precursor protein.";
RL Nat. Struct. Biol. 6:327-331(1999).
[17]
RN X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
RP MEDLINE=91104913; PubMed=2125487;
RX Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kosiakof A.A.;
RT "X-ray crystal structure of the protease inhibitor domain of
RT Alzheimer's amyloid beta-protein precursor.";
RL Biochemistry 29:10018-10022(1990).
[18]
RN STRUCTURE BY NMR OF 289-344.
RX MEDLINE=92031488; PubMed=1718421;
RA Heald S.L., Tilton R.F., Jr., Hammond L.S., Lee A., Bayney R.M.,
RA Kamarok M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
RA Tamburini P.P.;
RT "Sequential NMR resonance assignment and structure determination of
RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
RT precursor protein.";
RL Biochemistry 30:10467-10478(1991).
[19]
RN STRUCTURE BY NMR OF 672-699.
RX MEDLINE=94281210; PubMed=7516706;
RA Talafous J., Marciniowski K.J., Klopman G., Zagorski M.G.;
RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
RL Biochemistry 33:7788-7796(1994).
[20]
RN STRUCTURE BY NMR OF 696-706.
RX MEDLINE=97128622; PubMed=8973180;
RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
RT membrane-mimicking environment.";
RL Biochemistry 35:16094-16104(1996).
[21]
RN STRUCTURE BY NMR OF 672-711.
RX MEDLINE=98359783; PubMed=9693002;
RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscible
RT environment. Is the membrane-spanning domain where we think it is?";
RL Biochemistry 37:11064-11077(1998).
[22]
RN STRUCTURE BY NMR OF 672-699.
RX MEDLINE=20400066; PubMed=10940222;
RA Poulsen S.-A., Watson A.A., Craik D.J.;
RT "Solution structures in aqueous SDS micelles of two amyloid beta
RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
RT site.";
RL J. Struct. Biol. 130:142-152(2000).
[23]
RN STRUCTURE BY NMR OF 681-706.
RX MEDLINE=20400065; PubMed=10940221;
RA Zhang S., Iwata K., Lachenmann M.J., Peng J.W., Li S., Stimson E.R.,
RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;
RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in
RT water.";
RL J. Struct. Biol. 130:130-141(2000).
[24]
RN SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.

RA MEDLINE=88296437; PubMed=2900137;
RA Dyke T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.,
RT "Identification, Transmembrane orientation and biogenesis of the
RT amyloid A4 precursor of Alzheimer's disease.";
Query Match 100.0%; Score 54; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 KMDAEFRHDS 10
Db 670 KMDAEFRHDS 679
RESULT 9
A4_MOUSE STANDARD; PRT; 770 AA.
AC P12023;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (Ag).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC STRAIN-BALB/C; TISSUE-Brain;
RX MEDLINE=92096458; PubMed=1756177;
RA de Strooper B., van Leuven F., van den Bergh H.;
RT "The amyloid beta protein precursor or proteinase nexin II from mouse
RT is closer related to its human homolog than previously reported.";
RL Biochim. Biophys. Acta 1129:141-143(1991).
RN [2]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE-Brain;
RX MEDLINE=88106489; PubMed=3322280;
RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sasaki Y.;
RT "Complementary DNA for the mouse homolog of the human amyloid beta
RT protein precursor.";
RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN [3]
RP REVISIONS.
RA Yamada T.;
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 289-364 FROM N.A.
RC STRAIN-CD-1; TISSUE-Placenta;
RX MEDLINE=89345111; PubMed=2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RT precursor of Mus domestica.";
RL Nucleic Acids Res. 17:5396-5396(1989).
RN [5]
RP SEQUENCE OF 1-19 FROM N.A.
RX MEDLINE=92209998; PubMed=1555768;
RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA Sakai Y.;
RT "Positive and negative regulatory elements for the expression of the
RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL Gene 113:189-195(1992).
RN [6]
RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE-Brain, and Kidney;
RX MEDLINE=89149813; PubMed=2493250;
RA Yamada T., Sasaki H., Donura K., Goto I., Sasaki Y.;
RT Structure and expression of the alternatively-spliced forms of mRNA
RT for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor.";

RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
CC LIVER.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X59379; ?; NOT_ANNOTATED_CDS.
DR EMBL: M18373; AAA37139.1; -;
DR EMBL: X15210; CAA33280.1; -;
DR EMBL: D10603; BAA01456.1; -;
DR EMBL: M24597; AAA39929.1; -;
DR PIR: A27485; A27485.
DR PIR: S04855; S04855.
DR PIR: S19727; S19727.
DR HSSP: P05067; 10CM.
DR MCD: MGI:88059; APP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 770
FT FT
FT DOMAIN 18 699
FT TRANSMEM 700 723
FT DOMAIN 724 770
FT DOMAIN 673 715
FT DOMAIN 287 345
FT SITE 759 762
FT DISULFID 291 341
FT DISULFID 300 324
FT DISULFID 316 337
FT CARBOHYD 542 542
FT CARBOHYD 571 571
FT VARSPLIC 289 289
FT VARSPLIC 290 364
FT VARSPLIC 346 380
SQ SEQUENCE 770 AA; 86752 MW; 26C50DE0890CA7A CRC64;
Query Match 87.0%; Score 47; DB 1; Length 770;
Best Local Similarity 90.0%; Pred. No. 0.097;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 KMDAEFRHDS 10
||||| |||

DB 670 KMDAEFGHDS 679

RESULT 10

AA_RAT STANDARD: PRT; 770 AA.

ID A4_RAT

AC P08592;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog precursor (Amyloidogenic glycoprotein) (A β).

GN APP.

OS Rattus norvegicus (Rat);

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxId=10116;

OX

RN

RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=88312583; PubMed=2900758;

RA Shivers B.D., Hilbich C., Mulhaup G., Salbaum J.M., Beyreuther K., Seeburg P.H.;

RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.";

RL EMBO J. 7:1365-1370(1988).

RN [2]

RP SEQUENCE OF 289-364 FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=89183625; PubMed=2648331;

RA Kang J., Mueller-Hill B.;

RT "The sequence of the two extra exons in rat preA4.";

RL Nucleic Acids Res. 17:2130-2130(1989).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695), APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.

CC

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CC

DR EMBL: X07648; CA30488.1; -

DR EMBL: X14066; CA32229.1; -

DR PIR: S00550; S00550.

DR PIR: S03607; S03607.

DR HSSP: P05067; IAA.

DR InterPro: IPR001868; A4_APP.

DR InterPro: IPR002223; Kunitz_BPTI.

DR Pfam: PF02177; A4_EXTRA; 1.

DR Pfam: PF00014; Kunitz_BPTI; 1.

DR PRINTS: PR00203; AMYLOIDA4.

DR PRINTS: PR00759; BASICPTASE.

DR SMART: SM00006; A4_EXTRA; 1.

DR SMART: SM00131; KU; 1.

DR PROSITE: PS00319; A4_EXTRA; 1.

DR PROSITE: PS00320; A4_INTRA; 1.

DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.

DR Glycoprotein: Amyloid; Neurone; Transmembrane; Signal;

KM Alternative splicing; Serine protease inhibitor.

FT SIGNAL 1 17 BY SIMILARITY.

FT CHAIN 18 770 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN

FT DOMAIN 18 699 HOMOLOG.

FT TRANSMEM 700 723 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 724 770 POTENTIAL.

FT DOMAIN 673 715 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 287 345 EQUIVALENT OF BETA-AMYLOID PROTEIN.

FT SITE 759 762 BPTI/KUNITZ INHIBITOR.

FT DISULFID 291 341 CLATHRIN-BINDING (BY SIMILARITY).

FT DISULFID 300 324 BY SIMILARITY.

FT DISULFID 316 337 BY SIMILARITY.

FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPIC 289 289 E -> V (IN ISOFORM APP(695)).

FT VARSPIC 290 364 MISSING (IN ISOFORM APP(695)).

SO SEQUENCE 770 AA; 86704 MW; C26C9DBB2D929A7 CRC64;

Query Match 87.0%; Score 47; DB 1; Length 770;

Best Local Similarity 90.0%; Pred. No. 0.097;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KMDAEFGHDS 10

DB 670 KMDAEFGHDS 679

RESULT 11

COPD_BOVIN

ID COPD_BOVIN STANDARD: PRT; 511 AA.

AC P5619;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Coatomer delta subunit (delta-coat protein) (Delta-COP).

GN COPD.

OS Bos taurus (Bovine);

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OX NCBI_TaxId=9913;

RN [1]

RP SEQUENCE OF 2-511 FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=97011152; PubMed=8858162;

RA Faustlich D., Auerbach S., Orci L., Ravazzola M., Wegehingel S., Lutsepelch F., Stenbeck G., Harter C., Wieland F.T., Tschochner H.;

RT "Architecture of coatomer: molecular characterization of delta-COP and protein interactions within the complex.";

RL J. Cell Biol. 135:53-61(1996).

CC -1- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS TO DIVISIVE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER TRANSPORT OF DIVISIVE-TAGGED PROTEINS. IN MAMMALS, THE COATOMER CAN ONLY BE RECRUITED BY MEMBRANES ASSOCIATED TO ADP-RIBOSYLATION FACTORS (ARFs), WHICH ARE SMALL GTP-BINDING PROTEINS; THE COMPLEX ALSO INFLUENCES THE GOLGI STRUCTURAL INTEGRITY, AS WELL AS THE PROCESSING, ACTIVITY, AND ENDOCYTIC RECYCLING OF LDL RECEPTORS (BY SIMILARITY).

CC -1- SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA, BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.

CC -1- SUBCELLULAR LOCATION: THE COATOMER IS CYTOPLASMIC OR POLYMERIZED ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).

CC -1- TISSUE SPECIFICITY: UBIGUOUSLY EXPRESSED.

CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS FAMILY. COPD SUBFAMILY.

CC

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 CC -----
 DR EMBL: X94265; CAA63941.1; -
 DR InterPro: IPR001392; Adap_comp_sub.
 DR Pfam: PF00928; Adap_comp_sub; 1.
 KW Transport; Protein transport; Golgi stack; Membrane.
 SQ SEQUENCE 511 AA; 57274 MW; 6A285798F252CC7F CRC64;
 Query Match 72.2%; Score 39; DB 1; Length 511;
 Best Local Similarity 60.0%; Pred. No. 2.4;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KMDAEFRHDS 10
 Db 424 EIDGEXRHDS 433
 RESULT 12
 T2S1_STRFI
 ID T2S1_STRFI STANDARD; PRT; 511 AA.
 AC P48444;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Coatomer delta subunit (Delta-coat protein) (Delta-COP) (Archain).
 GN COPD OR ARCN1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=95301274; PubMed=7782067;
 RA Radice P., Pensotti V., Jones C., Perry H., Pierotti M.A.,
 RA Tunaciliffe A.;
 RT "The human archain gene, ARCN1, has highly conserved homologs in rice
 RT and Drosophila."
 RL Genomes 26:101-106(1995).
 CC -1- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS
 CC TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-
 CC CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC
 CC PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI
 CC NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI
 CC MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER
 CC TRANSPORT OF DILYSINE-TAGGED PROTEINS. IN MAMMALS, THE COATOMER
 CC CAN ONLY BE RECRUITED BY MEMBRANES ASSOCIATED TO ADP-RIBOSYLATION
 CC FACTORS (ARFs), WHICH ARE SMALL GTP-BINDING PROTEINS; THE COMPLEX
 CC ALSO INFLUENCES THE GOLGI STRUCTURAL INTEGRITY, AS WELL AS THE
 CC PROCESSING, ACTIVITY, AND ENDOCYTIC RECYCLING OF LDL RECEPTORS (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA,
 CC BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: THE COATOMER IS CYTOSOLIC OR POLYMERIZED
 CC ON THE CYTOSOLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE
 CC VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.
 CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
 CC FAMILY. COPD SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: X81197; CAA57071.1; -
 DR EMBL: X81198; CAA57072.1; ALT_INIT.
 DR MIM: 600820; -

DR InterPro: IPR001392; Adap_comp_sub.
 DR Pfam: PF00928; Adap_comp_sub; 1.
 KW Transport; Protein transport; Golgi stack; Membrane; Polymorphism.
 FT VARIANT 186 186 F->L (IN DBSNP:662327).
 FT FT /FTId=VAR_011788.
 FT VARIANT 309 309 K->N (IN DBSNP:1063124).
 FT /FTId=VAR_011789.
 SQ SEQUENCE 511 AA; 57210 MW; 4ED1F7D2D12A7E75 CRC64;
 Query Match 72.2%; Score 39; DB 1; Length 511;
 Best Local Similarity 60.0%; Pred. No. 2.4;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KMDAEFRHDS 10
 Db 424 EIDGEXRHDS 433
 RESULT 13
 T2S1_STRFI
 ID T2S1_STRFI STANDARD; PRT; 269 AA.
 AC O52512;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Type II restriction enzyme SfiI (EC 3.1.21.4) (Endonuclease SfiI)
 GN SFIIR.
 OS Streptomyces fluvialis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxId=66197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA van Cott E.M., Moran L.S., Slatko B.E., Wilson G.G.;
 RT "Characterization of the SfiI restriction and modification genes."
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE GCGCCNNNNNGCC
 CC AND CLEAVES BEFORE N-9.
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
 CC specific double-stranded fragments with terminal 5'-phosphates.
 CC -----
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 CC -----
 DR EMBL: AF039750; AAB95365.1; -
 DR REBASE: 1655; SfiI.
 DR Hydrolase; Endonuclease; Nuclease; Restriction system.
 SQ SEQUENCE 269 AA; 31044 MW; 3C48499BAA5205EA CRC64;
 Query Match 64.8%; Score 35; DB 1; Length 269;
 Best Local Similarity 77.8%; Pred. No. 7.7;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 MDAEFRHDS 10
 Db 119 MDAEFRHDS 127
 RESULT 14
 GIND_PSEAE
 ID GIND_PSEAE STANDARD; PRT; 900 AA.
 AC O929H0;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE [Protein-PiI] uridylyltransferase (EC 2.7.7.59) (PiI uridylyl-
 DE transferase) (Uridylyl removing enzyme) (UTase).

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 10:23:11 ; Search time 18 Seconds
(without alignments)
96.108 Million cell updates/sec

Title: US-09-580-018-7

Perfect score: 54

Sequence: 1 KMDAEFRHDS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rident:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	82	4	P78438
2	54	100.0	82	4	Q16014
3	54	100.0	82	4	Q16019
4	54	100.0	82	4	Q16020
5	54	100.0	534	13	Q93296
6	54	100.0	569	13	Q9PVL1
7	54	100.0	695	6	Q95KN7
8	54	100.0	695	11	Q60496
9	54	100.0	695	13	Q9DGJ8
10	54	100.0	751	13	Q9DGJ7
11	54	100.0	770	6	Q9RTU0
12	47	87.0	79	11	Q35463
13	47	87.0	607	11	Q99K32
14	47	87.0	693	11	P97487
15	45	83.3	693	13	Q98S60
16	45	83.3	695	13	Q98SP9

17	45	83.3	747	13	Q91963	Q91963 xenopus, ap
18	44	81.5	19	4	Q9UC68	Q9UC68 homo sapien
19	44	81.5	28	4	Q9UCD1	Q9UCD1 homo sapien
20	44	81.5	30	4	Q9UCAD	Q9UCAD homo sapien
21	44	81.5	33	4	Q9UC33	Q9UC33 homo sapien
22	40	74.1	423	2	Q45693	Q45693 raltosonia s
23	40	74.1	423	2	Q45693	Q45693 burkholderi
24	39	72.2	511	11	Q91M48	Q91M48 mus musculu
25	37	66.5	418	2	Q9KY96	Q9KY96 streptomyce
26	36	66.5	755	5	Q9VF30	Q9VF30 drosophila
27	35	64.8	428	16	Q912U4	Q912U4 pseudomonas
28	35	64.8	543	10	Q9LZL4	Q9LZL4 arabidopsis
29	35	64.8	802	16	Q9HML3	Q9HML3 pseudomonas
30	34	63.0	97	4	Q13778	Q13778 homo sapien
31	34	63.0	206	2	Q44945	Q44945 borrelia bu
32	34	63.0	210	2	Q93MK6	Q93MK6 vibrio vuln
33	34	63.0	213	16	Q9A314	Q9A314 caulobacter
34	34	63.0	229	10	Q9LUF9	Q9LUF9 arabidopsis
35	34	63.0	240	16	Q92PX4	Q92PX4 rhizobium m
36	34	63.0	265	2	Q9AOL8	Q9AOL8 pseudomonas
37	34	63.0	329	17	Q9HMG1	Q9HMG1 halobacteri
38	34	63.0	347	12	Q91FD6	Q91FD6 chilo iride
39	34	63.0	399	12	Q9QB65	Q9QB65 wheat yellow
40	34	63.0	400	2	Q52295	Q52295 shigella fl
41	34	63.0	431	2	Q935K0	Q935K0 salmonella
42	34	63.0	432	2	Q93RK7	Q93RK7 bacillus sp
43	34	63.0	439	2	Q915T6	Q915T6 salmonella
44	34	63.0	452	11	Q91ZK0	Q91ZK0 mus musculu
45	34	63.0	555	12	Q9QBG3	Q9QBG3 wheat yellow

ALIGNMENTS

RESULT 1
ID P78438 PRELIMINARY; PRT; 82 AA.
AC P78438;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
[2]
RP SEQUENCE OF 19-48 FROM N.A.
RX MEDLINE=87120329; PubMed=2949367;
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
RT linkage near the Alzheimer locus.";
RL Science 235:880-884(1987).
[3]
RP SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE=93035397; PubMed=1415269;
RA Kamlin K., Orr H.T., Payami H., Wajsbom E.M., Alonso M.E., Pulst S.M.,
RA Anderson L., O'dahl S., Nemens E., White J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease
RT kindreds for the APP gene region.";
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL; M29270; AAA51768.1; -.
DR EMBL; M29269; AAA51768.1; JOINED.

DR EMBL: M15532; AAA51564.1; -.
 DR EMBL: S45136; AAB23646.1; -.
 DR HSSP: P05067; 1BA4.
 FT NON_TER 1
 SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match
 Best Local Similarity 100.0%; Score 54; DB 4; Length 82;
 Pred. No. 0.0017;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10
 DB 15 KMDAEFRHDS 24

RESULT 2
 Q16014 PRELIMINARY; PRT; 82 AA.
 AC Q16014;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE BETA-AMYLLOID PEPTIDE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93236601; PubMed=8476439;
 RA Denman R.B., Rosenzwaig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor."
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 DR EMBL: S60721; AAB26253.2; -.
 DR HSSP: P05067; 1BA4.
 FT NON_TER 1
 SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match
 Best Local Similarity 100.0%; Score 54; DB 4; Length 82;
 Pred. No. 0.0017;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10
 DB 16 KMDAEFRHDS 25

RESULT 3
 Q16019 PRELIMINARY; PRT; 82 AA.
 AC Q16019;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE BETA-AMYLLOID PEPTIDE (FRAGMENT).
 GN BETA APP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93236601; PubMed=8476439;
 RA Denman R.B., Rosenzwaig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor."
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 DR EMBL: S61380; AAB26264.2; -.
 DR HSSP: P05067; 1BA4.
 FT NON_TER 1
 SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match
 Best Local Similarity 100.0%; Score 54; DB 4; Length 82;
 Pred. No. 0.0017;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10
 DB 16 KMDAEFRHDS 25

RESULT 4
 Q16020 PRELIMINARY; PRT; 82 AA.
 AC Q16020;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE BETA-AMYLLOID PEPTIDE (FRAGMENT).
 GN BETA APP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93236601; PubMed=8476439;
 RA Denman R.B., Rosenzwaig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor."
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 DR EMBL: S61383; AAB26255.2; -.
 DR HSSP: P05067; 1BA4.
 FT NON_TER 1
 SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match
 Best Local Similarity 100.0%; Score 54; DB 4; Length 82;
 Pred. No. 0.0017;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMDAEFRHDS 10
 DB 16 KMDAEFRHDS 25

RESULT 5
 Q93296 PRELIMINARY; PRT; 534 AA.
 AC Q93296;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE AMYLLOID PROTEIN (FRAGMENT).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9637885; PubMed=9671674;
 RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W., Milligan C.E.;
 RT "Increased production of amyloid precursor protein provides a substrate for caspase-3 in dying motoneurons."
 RL J. Neurosci. 18:5869-5880(1998).
 DR EMBL: AF042098; AAC25052.1; -.
 DR HSSP: P05067; 1BA4.
 DR InterPro: IPR001868; A4_APP.
 DR PRINTS: PRO0203; AMYLLOID4.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.

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FT NON_TER 1 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;
Query Match
Best Local Similarity 100.0%; Score 54; DB 13; Length 534;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAERRHDS 10
    |||||||
Db 434 KMDAERRHDS 443

RESULT 6
O9PVL1 PRELIMINARY; PRT; 569 AA.
AC O9PVL1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA Coulson E.J., Paliaga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RL tells us about its function.";
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12698.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;
Query Match
Best Local Similarity 100.0%; Score 54; DB 13; Length 569;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAERRHDS 10
    |||||||
Db 470 KMDAERRHDS 479

RESULT 7
O9SKN7 PRELIMINARY; PRT; 695 AA.
AC O9SKN7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AMYLOID B-PROTEIN PRECURSOR.
OS Macaca fascicularis (Crah eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RC MEDLINE=91273117; PubMed=1905108;
RA Podlasky M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's

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RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).
DR EMBL; M58727; AAA36829.1; -.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 597 636 POTENTIAL.
SO SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;
Query Match
Best Local Similarity 100.0%; Score 54; DB 6; Length 695;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAERRHDS 10
    |||||||
Db 595 KMDAERRHDS 604

RESULT 8
O60496 PRELIMINARY; PRT; 695 AA.
AC O60496;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE POTATIVE AMYLOID PRECURSOR PROTEIN.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RC MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing.";
RL Blochim. Biophys. Acta 1351:17-21(1997).
DR EMBL; X97631; CAA66230.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;
Query Match
Best Local Similarity 100.0%; Score 54; DB 11; Length 695;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAERRHDS 10
    |||||||
Db 595 KMDAERRHDS 604

RESULT 9
O9DCJ8 PRELIMINARY; PRT; 695 AA.
AC O9DCJ8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOROM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolosse A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms.";

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RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289218; AAC00593.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match
Best Local Similarity 100.0%; Score 54; DB 13; Length 695;
Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
DB 595 KMDAEFRHDS 604

RESULT 10
O9DGJ7 PRELIMINARY; PRT; 751 AA.
AC O9DGJ7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolosse A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289219; AAC00594.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match
Best Local Similarity 100.0%; Score 54; DB 13; Length 751;
Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
DB 651 KMDAEFRHDS 660

RESULT 11
O9TU10 PRELIMINARY; PRT; 770 AA.
AC O9TU10;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid precursor Protein 770.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB032550; BAA84580.1; -.
DR HSSP: P05067; 1AAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BCC583E CRC64;

Query Match
Best Local Similarity 100.0%; Score 54; DB 6; Length 770;
Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
DB 670 KMDAEFRHDS 679

RESULT 12
O35463 PRELIMINARY; PRT; 79 AA.
AC O35463;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).
DE BETA APP.
GN Cricetus griseus (Chinese hamster).
OC Cricetidae; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarnbanurci K., Pinnix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF030413; AAB86608.1; -.
DR HSSP: P05067; 1BA4.
DR FT NON_TER 1 79
FT NON_TER 1 79
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match
Best Local Similarity 90.0%; Score 47; DB 11; Length 79;
Pred. No. 0.041;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
DB 19 KMDAEFRHDS 28

RESULT 13
O99K32 PRELIMINARY; PRT; 607 AA.
AC O99K32;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE HYPOTHETICAL 68.4 KDA PROTEIN (FRAGMENT).
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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RC TISSUE.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005490; AAH05490.1; -.
DR HSSP; P05067; 1AAP.
DR InterPro; IPR001868; Kunitz-BPTI.
DR InterPro; IPR002223; Kunitz-BPTI.
DR Pfam; PF00014; Kunitz-BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Hypothetical protein; Serine protease inhibitor.
FT NON_TER
SO SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;

Query Match
Best Local Similarity 87.0%; Score 47; DB 11; Length 607;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
DB 507 KMDAEFRHDS 516

RESULT 14
P97487 PRELIMINARY; PRT; 695 AA.
AC P97487; P97942;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HIPPOCAMPAL AMYLOID PROTEIN.
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SAMP8; TISSUE=HIPPOCAMPUS;
RA Flood J.F.; Kumar V.B.; Sasser T.; Word I.; Morley J.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 581-662 FROM N.A.
RC STRAIN=129SV;
RA Wragg M.A.; Busfield F.; Duff K.; Korenblat K.; Capechi M.;
RL Loring J.F.; Goate A.M.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U84012; AAB41502.1; -.
DR HSSP; P05067; 1AMP.
DR MGD; MGI:88059; APP.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SO SEQUENCE 695 AA; 78414 MW; 9A5FBE2ED261236E CRC64;

Query Match
Best Local Similarity 87.0%; Score 47; DB 11; Length 695;
Matches 9; Conservative 90.0%; Pred. No. 0.44;

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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
DB 595 KMDAEFRHDS 604

RESULT 15
O98SGO PRELIMINARY; PRT; 693 AA.
AC O98SGO;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN A.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OX Xenopodinae; Xenopus.
OX NCBI_TaxID=8395;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL; AJ298150; CAC37193.1; -.
DR HSSP; P05067; 1H23.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW Signal.
FT SIGNAL
SO SEQUENCE 693 AA; 78568 MW; CAFIDF655C1AB653 CRC64;

Query Match
Best Local Similarity 83.3%; Score 45; DB 13; Length 693;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 KMDAEFRHDS 10
DB 593 KMDSEYRHDT 602

Search completed: October 29, 2002, 10:29:44
Job time : 19.1429 secs

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